

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Yurieva, Olga
Kuriyan, John
O'Donnell, Michael E.
Jeruzalmi, David
- (ii) TITLE OF INVENTION: ENZYME DERIVED FROM THERMOPHILIC ORGANISMS
THAT FUNCTIONS AS A CHROMOSOMAL REPLICASE, PREPARATION AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 116
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: David A. Jackson, Esq.
(B) STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/US
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/143,202
(B) FILING DATE: 08-APR-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/823,407
(B) FILING DATE: 08-APR-1997
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Jackson Esq., David A.
(B) REGISTRATION NUMBER: 26,742
(C) REFERENCE/DOCKET NUMBER: 600-1-179 PCT
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 201-487-5800
(B) TELEFAX: 201-343-1684

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2007 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

004233.024960

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- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/143,202
(B) FILING DATE: 08-APR-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/823,407
(B) FILING DATE: 08-APR-1997
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- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Jackson Esq., David A.
(B) REGISTRATION NUMBER: 26,742
(C) REFERENCE/DOCKET NUMBER: 600-1-179 N
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 201-487-5800
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2007 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

008780 "B224360

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCCGGGGGTG	GGGTTCCCAG	GTAGACCCCG	GCCCCTCCCG	TGAGCCCCTT	TACCCAGGCC	60
GCCACCTCCT	CCAGGGGGGC	CAAGGCGTGC	AAGGAGAGGA	ACGTCCGCAC	CACGCCCTAT	120
ACTAGCCTTG	TGAGCGCCCT	CTACCGCCGC	TTCCGCCCCC	TCACCTTCCA	GGAGGTGGTG	180
GGGCAGGAGC	ACGTGAAGGA	GCCCCCTCCTC	AAGGCCATCC	GGGAGGGGAG	GCTCGCCCAG	240
GCCTACCTCT	TCTCCGGGCC	CAGGGGCGTG	GGCAAGACCA	CCACGGCGAG	GCTCCTCGCC	300
ATGGCGGTGG	GGTGCCAGGG	GGAAGACCCC	CCTTGCGGGG	TCTGCCCCCA	CTGCCAGGCG	360
GTGCAGAGGG	GCGCCCACCC	GGACGTGGTG	GACATTGACG	CCGCCAGCAA	CAACTCCGTG	420
GAGGACGTGC	GGGAGCTGAG	GGAAAGGATC	CACCTCGCCC	CCCTCTCTGC	CCCCAGGAAG	480
GTCTTCATCC	TGGACGAGGC	CCACATGCTC	TCCAAAAGCG	CCTTCAACGC	CCTCCTCAAG	540
ACCCTGGAGG	AGCCCCCGCC	CCACGTCCCTC	TTCGTCTTCG	CCACCACCGA	GCCCCGAGAGG	600
ATGCCCCCCA	CCATCCTCTC	CCGCACCCAG	CACTTCCGCT	TCCGCCGCCT	CACGGAGGAG	660
GAGATCGCCT	TTAAGCTCCG	GCGCATCCTG	GAGGCCGTGG	GGCGGGAGGC	GGAGGAGGAG	720
GCCCTCCTCC	TCCTCGCCCG	CCTGGCGGAC	GGGGCCCTTA	GGGACGCGGA	AAGCCTCCTG	780
GAGCGCTTCC	TCCTCCTGGA	AGGCCCCCTC	ACCCGGAAGG	AGGTGGAGCG	CGCCCTAGGC	840
TCCCCCCCAG	GGACCGGGGT	GGCCGAGATC	GCCGCCTCCC	TCGCGAGGGG	GAAAACGGCG	900
GAGGCCCTGG	GCCTCGCCCG	GCGCCTCTAC	GGGAAGGGT	ACGCCCCGAG	GAGCCTGGTC	960
TCGGGCCTTT	TGGAGGTGTT	CCGGGAAGGC	CTCTACGCCG	CCTTCGGCCT	CGCGGGAACC	1020
CCCCTTCCCG	CCCCGCCCCA	GGCCCTGATC	GCCGCCATGA	CCGCCCTGGA	CGAGGCCATG	1080
GAGCGCCTCG	CCCGCCGCTC	CGACGCCTTA	AGCCTGGAGG	TGGCCCTCCT	GGAGGCGGGA	1140
AGGGCCCTGG	CCGCCGAGGC	CCTACCCCAG	CCCACGGGCG	CTCCTTCCCC	AGAGGTCGGC	1200
CCCAAGCCGG	AAAGCCCCCC	GACCCCGGAA	CCCCCAAGGC	CCGAGGAGGC	GCCCCGACCTG	1260
CGGGAGCGGT	GGCGGGCCTT	CCTCGAGGCC	CTCAGGCCCA	CCCTACGGGC	CTTCGTGCGG	1320
GAGGCCCGCC	CGGAGGTCCG	GGAAGGCCAG	CTCTGCCTCG	CTTTCCCCGA	GGACAAGGCC	1380
TTCCACTACC	GCAAGGCCTC	GGAACAGAAG	GTGAGGCTCC	TCCCCCTGGC	CCAGGCCCAT	1440
TTCGGGGTGG	AGGAGGTCGT	CCTCGTCCTG	GAGGGAGAAA	AAAAAAGCCT	GAGCCCAAGG	1500
CCCCGCCCCG	CCCCACCTCC	TGAAGCGCCC	GCACCCCGG	GCCCTCCCGA	GGAGGAGGTA	1560
GAGGCGGAGG	AAGCGGCGGA	GGAGGCCCCG	GAGGAGGCCT	TGAGGCGGGT	GGTCCGCCTC	1620

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CTGGGGGGGC GGGTGCTCTG GCGGCGG CCCAGGACCC GGGAGGCGCC GGAGGAGGAA 1680
 CCCCTGAGCC AAGACGAGAT AGGGGGTACT GGTATATAAT GGGGGCATGA CGCGGACCAC 1740
 CGACCTCGGA CAAGAGACCG TGGACAACAT CCTCAAGCGC CTCCGCCGTA TTGAGGGCCA 1800
 GGTGCGGGGG CTCCAGAAGA TGGTGCCGA GGGCCGCCCC TGCACGAGG TCCTCACCCA 1860
 GATGACCGCC ACCAAGAAGG CCATGGAGGC GCGGCCACC CTGATCCTCC ACGAGTTCCT 1920
 GAACGTCTGC GCCGCCGAGG TCTCCGAGGG CAAGGTGAAC CCCAAGAAGC CCGAGGAGAT 1980
 CGCCACCATG CTGAAGAACT TCATCTA 2007

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 529 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Ala	Leu	Tyr	Arg	Arg	Phe	Arg	Pro	Leu	Thr	Phe	Gln	Glu	Val
1				5					10					15	
Val	Gly	Gln	Glu	His	Val	Lys	Glu	Pro	Leu	Leu	Lys	Ala	Ile	Arg	Glu
			20					25					30		
Gly	Arg	Leu	Ala	Gln	Ala	Tyr	Leu	Phe	Ser	Gly	Pro	Arg	Gly	Val	Gly
		35					40					45			
Lys	Thr	Thr	Thr	Ala	Arg	Leu	Leu	Ala	Met	Ala	Val	Gly	Cys	Gln	Gly
	50					55					60				
Glu	Asp	Pro	Pro	Cys	Gly	Val	Cys	Pro	His	Cys	Gln	Ala	Val	Gln	Arg
65				70					75					80	
Gly	Ala	His	Pro	Asp	Val	Val	Asp	Ile	Asp	Ala	Ala	Ser	Asn	Asn	Ser
			85					90					95		
Val	Glu	Asp	Val	Arg	Glu	Leu	Arg	Glu	Arg	Ile	His	Leu	Ala	Pro	Leu
		100					105					110			
Ser	Ala	Pro	Arg	Lys	Val	Phe	Ile	Leu	Asp	Glu	Ala	His	Met	Leu	Ser
	115						120					125			
Lys	Ser	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	Glu	Pro	Pro	Pro
	130				135						140				
His	Val	Leu	Phe	Val	Phe	Ala	Thr	Thr	Glu	Pro	Glu	Arg	Met	Pro	Pro
145					150				155					160	

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Leu Leu Gly Gly Ala Val Leu Trp Val Arg Arg Pro Arg Thr Arg Glu
500 505 510

Ala Pro Glu Glu Glu Pro Leu Ser Gln Asp Glu Ile Gly Gly Thr Gly
515 520 525

Ile

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTGAGCGCCC TCTACGCCG CTTCCGCCCC CTCACCTTCC AGGAGGTGGT GGGGCAGGAG	60
CACGTGAAGG AGCCCCCTCT CAAGGCCATC CGGGAGGGGA GGCTCGCCCA GGCCTACCTC	120
TTCTCCGGGC CCAGGGGCGT GGGCAAGACC ACCACGGCGA GGCTCCTCGC CATGGCGGTG	180
GGGTGCCAGG GGAAGACCC CCCTTGCGGG GTCTGCCCC ACTGCCAGGC GGTGCAGAGG	240
GGCGCCACC CGGACGTGGT GGACATTGAC GCCGCCAGCA ACAACTCCGT GGAGGACGTG	300
CGGGAGCTGA GGAAGGAT CCACCTCGCC CCCCTCTCTG CCCCAGGAA GGTCTTCATC	360
CTGGACGAGG CCCACATGCT CTCCAAAAGC GCCTTCAACG CCCTCCTCAA GACCCTGGAG	420
GAGCCCCCGC CCCACGTCTT CTTCGTCTTC GCCACCACCG AGCCCAGAG GATGCCCCC	480
ACCATCCTCT CCCGCACCCA GCACTTCCGC TTCCGCCGCC TCACGGAGGA GGAGATCGCC	540
TTTAAGCTCC GCGCATCCT GGAGGCCGTG GGGCGGGAGG CGGAGGAGGA GGCCCTCCTC	600
CTCCTCGCCC GCCTGGCGGA CGGGGCCCTT AGGGACGCGG AAAGCCTCCT GGAGCGCTTC	660
CTCCTCCTGG AAGGCCCCCT CACCCGGAAG GAGGTGGAGC GCGCCCTAGG CTCCCCC	720
GGGACCGGGG TGGCCGAGAT CGCCGCCTCC CTCGCGAGGG GGAAAACGGC GGAGGCCCTG	780
GGCCTCGCCC GGCGCCTCTA CGGGGAAGGG TACGCCCCGA GGAGCCTGGT CTCGGGCCTT	840
TTGGAGGTGT TCCGGGAAGG CCTCTACGCC GCCTTCGGCC TCGCGGAAC CCCCCTTCCC	900
GCCCCGCCCC AGGCCCTGAT CGCCGCCATG ACCGCCCTGG ACGAGGCCAT GGAGCGCCTC	960
GCCCCGCGCT CCGACGCCTT AAGCCTGGAG GTGGCCCTCC TGGAGGCGGG AAGGGCCCTG	1020
GCCGCCGAGG CCCTACCCCA GCCCACGGGC GCTCCTTCCC CAGAGGTCGG CCCCAAGCCG	1080

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GAAAGCCCC CGACCCCGGA ACCCCCAAGG CCCGAGGAGG CGCCCGACCT GCGGGAGCGG 1140
 TGGCGGGCCT TCCTCGAGGC CCTCAGGCCC ACCCTACGGG CCTTCGTGCG GGAGGCCCCG 1200
 CCGGAGGTCC GGAAGGCCA GCTCTGCCTC GCTTTCCCCG AGGACAAGGC CTTCCACTAC 1260
 CGCAAGGCCT CGGAACAGAA GGTGAGGCTC CTCCCCCTGG CCCAGGCCCA TTTCGGGGTG 1320
 GAGGAGGTCTG TCCTCGTCCT GGAGGGAGAA AAAAAAGCC TGAGCCCAAG GCCCCGCCCG 1380
 GCCCCACCTC CTGAAGCGCC CGCACCCCG GGCCTCCCG AGGAGGAGGT AGAGGCGGAG 1440
 GAAGCGCGG AGGAGGCCCC GGAGGAGGCC TTGAGGCGGG TGGTCCGCCT CCTGGGGGGG 1500
 CGGGTGCTCT GGGTGCGGCG GCCCAGGACC CGGGAGGCGC CGGAGGAGGA ACCCCTGAGC 1560
 CAAGACGAGA TAGGGGTAC TGGTATATAA 1590

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 464 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Ala	Leu	Tyr	Arg	Arg	Phe	Arg	Pro	Leu	Thr	Phe	Gln	Glu	Val
1				5					10					15	
Val	Gly	Gln	Glu	His	Val	Lys	Glu	Pro	Leu	Leu	Lys	Ala	Ile	Arg	Glu
			20					25					30		
Gly	Arg	Leu	Ala	Gln	Ala	Tyr	Leu	Phe	Ser	Gly	Pro	Arg	Gly	Val	Gly
		35					40					45			
Lys	Thr	Thr	Thr	Ala	Arg	Leu	Leu	Ala	Met	Ala	Val	Gly	Cys	Gln	Gly
	50					55					60				
Glu	Asp	Pro	Pro	Cys	Gly	Val	Cys	Pro	His	Cys	Gln	Ala	Val	Gln	Arg
65				70					75					80	
Gly	Ala	His	Pro	Asp	Val	Val	Asp	Ile	Asp	Ala	Ala	Ser	Asn	Asn	Ser
				85				90						95	
Val	Glu	Asp	Val	Arg	Glu	Leu	Arg	Glu	Arg	Ile	His	Leu	Ala	Pro	Leu
			100					105					110		
Ser	Ala	Pro	Arg	Lys	Val	Phe	Ile	Leu	Asp	Glu	Ala	His	Met	Leu	Ser
		115					120					125			
Lys	Ser	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	Glu	Pro	Pro	Pro

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130	135	140
His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro 145 150 155 160		
Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu 165 170 175		
Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg 180 185 190		
Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly 195 200 205		
Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu 210 215 220		
Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro 225 230 235 240		
Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr 245 250 255		
Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala 260 265 270		
Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu 275 280 285		
Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln 290 295 300		
Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu 305 310 315 320		
Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala 325 330 335		
Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro 340 345 350		
Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro 355 360 365		
Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe 370 375 380		
Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg 385 390 395 400		
Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys 405 410 415		
Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro 420 425 430		
Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu 435 440 445		
Gly Glu Lys Lys Lys Pro Glu Pro Lys Ala Pro Pro Gly Pro Thr Ser 450 455 460		

(2) INFORMATION FOR SEQUENCE NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ser	Ala	Leu	Tyr	Arg	Arg	Phe	Arg	Pro	Leu	Thr	Phe	Gln	Glu	Val
1				5					10					15	
Val	Gly	Gln	Glu	His	Val	Lys	Glu	Pro	Leu	Leu	Lys	Ala	Ile	Arg	Glu
			20					25					30		
Gly	Arg	Leu	Ala	Gln	Ala	Tyr	Leu	Phe	Ser	Gly	Pro	Arg	Gly	Val	Gly
			35				40					45			
Lys	Thr	Thr	Thr	Ala	Arg	Leu	Leu	Ala	Met	Ala	Val	Gly	Cys	Gln	Gly
	50					55					60				
Glu	Asp	Pro	Pro	Cys	Gly	Val	Cys	Pro	His	Cys	Gln	Ala	Val	Gln	Arg
65					70					75					80
Gly	Ala	His	Pro	Asp	Val	Val	Asp	Ile	Asp	Ala	Ala	Ser	Asn	Asn	Ser
				85					90					95	
Val	Glu	Asp	Val	Arg	Glu	Leu	Arg	Glu	Arg	Ile	His	Leu	Ala	Pro	Leu
			100					105					110		
Ser	Ala	Pro	Arg	Lys	Val	Phe	Ile	Leu	Asp	Glu	Ala	His	Met	Leu	Ser
		115					120					125			
Lys	Ser	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	Glu	Pro	Pro	Pro
	130					135					140				
His	Val	Leu	Phe	Val	Phe	Ala	Thr	Thr	Glu	Pro	Glu	Arg	Met	Pro	Pro
145					150					155					160
Thr	Ile	Leu	Ser	Arg	Thr	Gln	His	Phe	Arg	Phe	Arg	Arg	Leu	Thr	Glu
				165					170					175	
Glu	Glu	Ile	Ala	Phe	Lys	Leu	Arg	Arg	Ile	Leu	Glu	Ala	Val	Gly	Arg
			180					185					190		
Glu	Ala	Glu	Glu	Glu	Ala	Leu	Leu	Leu	Leu	Ala	Arg	Leu	Ala	Asp	Gly
		195					200					205			
Ala	Leu	Arg	Asp	Ala	Glu	Ser	Leu	Leu	Glu	Arg	Phe	Leu	Leu	Leu	Glu
	210					215					220				
Gly	Pro	Leu	Thr	Arg	Lys	Glu	Val	Glu	Arg	Ala	Leu	Gly	Ser	Pro	Pro
225					230					235					240

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Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
 245 250 255
 Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
 260 265 270
 Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
 275 280 285
 Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
 290 295 300
 Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
 305 310 315 320
 Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
 325 330 335
 Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
 340 345 350
 Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
 355 360 365
 Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
 370 375 380
 Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
 385 390 395 400
 Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
 405 410 415
 Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
 420 425 430
 Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
 435 440 445
 Gly Glu Lys Lys Lys Ala
 450

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
- (A) DESCRIPTION: /desc = "Primer"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGCAAGCTTC ACGCNTACCT NTTCTCCGGN AC

[illegible]

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

His Ala Tyr Leu Phe Ser Gly Thr
1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Primer"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCGAATTCG TGCTCNGGNG GCTCCTCNAG NGTC

34

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- PHYSICAL CHARACTERISTICS:
- (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys Thr Leu Glu Glu Pro Pro Glu His
1 5

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCGCGGATCC GGAGGGAGAA AAAAAAGCC TCAGCCCA

38

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCGCGGATCC GGAGGGAGAG AAGAAAAGCC TCAGCCCA

38

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAATTAAATT CGCGCTTCGG GAGGTGGG

28

(2) INFORMATION FOR SEQ ID NO:13:

00642219 081800

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Primer"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
GCGCGAATTC GCGCTTCGGG AGGTGGG

27

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Primer"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
GCGCGAATTC GGGCGCTTCA GGAGGTGGG

29

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Primer"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
GTGGTGCATA TGGTGAGCGC CCTCTACCGC C

31

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid

00642218 "081800

[illegible]

(iii) HYPOTHETICAL: NO

GTGGTGGTCG ACCCAGGAGG GCCACCTCCA G

31

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

Gly Xaa Xaa Gly Xaa Gly Lys Thr
1 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

Lys Pro Asp Pro Lys Ala Pro Pro Gly Pro Thr Ser
1 5 10

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 amino acids

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

(2) INFORMATION FOR SEQ ID NO:20:

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

THE UNIVERSITY OF CHICAGO

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEO ID NO:21:

Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Gln Thr Phe Ala

00642218-08400

1	5	10	15
Asp Val Val Gly Gln Glu His Val Leu Thr Ala Leu Ala Asn Gly Leu	20	25	30
Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly	35	40	45
Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys	50	55	60
Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg	65	70	75
Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala	85	90	95
Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln	100	105	110
Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val	115	120	125
His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu	130	135	140
Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln	145	150	155
Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys	165	170	175
Ala Leu Asp Val Glu Gln Ile Arg His Gln Leu Glu His Ile Leu Asn	180	185	190
Glu Glu His Ile Ala His Glu Pro Arg Ala Leu Gln Leu Leu Ala Arg	195	200	205
Ala Ala Glu Gly Ser Leu Arg Asp Ala Leu Ser Leu Thr Asp Gln Ala	210	215	220
Ile Ala Ser Gly Asp Gly Gln Val Ser Thr Gln Ala Val Ser Ala Met	225	230	235
Leu Gly Thr Leu Asp Asp Asp Gln Ala Leu Ser Leu Val Glu Ala Met	245	250	255
Val Glu Ala Asn Gly Glu Arg Val Met Ala Leu Ile Asn Glu Ala Ala	260	265	270
Ala Arg Gly Ile Glu Trp Glu Ala Leu Leu Val Glu Met Leu Gly Leu	275	280	285
Leu His Arg Ile Ala Met	290		

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Ser	Tyr	Gln	Val	Leu	Ala	Arg	Lys	Trp	Arg	Pro	Lys	Thr	Phe	Ala	1	5	10	15
Asp	Val	Val	Gly	Gln	Glu	His	Ile	Ile	Thr	Ala	Leu	Ala	Asn	Gly	Leu	20	25	30	
Lys	Asp	Asn	Arg	Leu	His	His	Ala	Tyr	Leu	Phe	Ser	Gly	Thr	Arg	Gly	35	40	45	
Val	Gly	Lys	Thr	Ser	Ile	Ala	Arg	Leu	Phe	Ala	Lys	Gly	Leu	Asn	Cys	50	55	60	
Val	His	Gly	Val	Thr	Ala	Thr	Pro	Cys	Gly	Glu	Cys	Glu	Asn	Cys	Lys	65	70	75	80
Ala	Ile	Glu	Gln	Gly	Asn	Phe	Ile	Asp	Leu	Ile	Glu	Ile	Asp	Ala	Ala	85	90	95	
Ser	Arg	Thr	Lys	Val	Glu	Asp	Thr	Arg	Glu	Leu	Leu	Asp	Asn	Val	Gln	100	105	110	
Tyr	Lys	Pro	Val	Val	Gly	Arg	Phe	Lys	Val	Tyr	Leu	Ile	Asp	Glu	Val	115	120	125	
His	Met	Leu	Ser	Arg	His	Ser	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	130	135	140	
Glu	Pro	Pro	Glu	Tyr	Val	Lys	Phe	Leu	Leu	Ala	Thr	Thr	Asp	Pro	Gln	145	150	155	160
Lys	Leu	Pro	Val	Thr	Ile	Leu	Ser	Arg	Cys	Leu	Gln	Phe	His	Leu	Lys	165	170	175	
Ala	Leu	Asp	Glu	Thr	Gln	Ile	Ser	Gln	His	Leu	Ala	His	Ile	Leu	Thr	180	185	190	
Gln	Glu	Asn	Ile	Pro	Phe	Glu	Asp	Pro	Ala	Leu	Val	Lys	Leu	Ala	Lys	195	200	205	
Ala	Ala	Gln	Gly	Ser	Ile	Arg	Asp	Ser	Leu	Ser	Leu	Thr	Asp	Gln	Ala	210	215	220	
Ile	Ala	Met	Gly	Asp	Arg	Gln	Val	Thr	Asn	Asn	Val	Val	Ser	Asn	Met	225	230	235	240
Leu	Gly	Leu	Leu	Asp	Asp	Asn	Tyr	Ser	Val	Asp	Ile	Leu	Tyr	Ala	Leu	245	250	255	
His	Gln	Gly	Asn	Gly	Glu	Leu	Leu	Met	Arg	Thr	Leu	Gln	Arg	Val	Ala	260	265	270	

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Asp Ala Ala Gly Asp Trp Asp Lys Leu Leu Gly Glu Cys Ala Glu Lys
 275 280 285

Leu His Gln Ile Ala Leu
 290

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Ser	Tyr	Gln	Ala	Leu	Tyr	Arg	Val	Phe	Arg	Pro	Gln	Arg	Phe	Glu	1	5	10	15
Asp	Val	Val	Gly	Gln	Glu	His	Ile	Thr	Lys	Thr	Leu	Gln	Asn	Ala	Leu	20	25	30	
Leu	Gln	Lys	Lys	Phe	Ser	His	Ala	Tyr	Leu	Phe	Ser	Gly	Pro	Arg	Gly	35	40	45	
Thr	Gly	Lys	Thr	Ser	Ala	Ala	Lys	Ile	Phe	Ala	Lys	Ala	Val	Asn	Cys	50	55	60	
Glu	His	Ala	Pro	Val	Asp	Glu	Pro	Cys	Asn	Glu	Cys	Ala	Ala	Cys	Lys	65	70	75	80
Gly	Ile	Thr	Asn	Gly	Ser	Ile	Ser	Asp	Val	Ile	Glu	Ile	Asp	Ala	Ala	85	90	95	
Ser	Asn	Asn	Gly	Val	Asp	Glu	Ile	Arg	Asp	Ile	Arg	Asp	Lys	Val	Lys	100	105	110	
Phe	Ala	Pro	Ser	Ala	Val	Thr	Tyr	Lys	Val	Tyr	Ile	Ile	Asp	Glu	Val	115	120	125	
His	Met	Leu	Ser	Ile	Gly	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	130	135	140	
Glu	Pro	Pro	Glu	His	Cys	Ile	Phe	Ile	Leu	Ala	Thr	Thr	Glu	Pro	His	145	150	155	160
Lys	Ile	Pro	Leu	Thr	Ile	Ile	Ser	Arg	Cys	Gln	Arg	Phe	Asp	Phe	Lys	165	170	175	
Arg	Ile	Thr	Ser	Gln	Ala	Ile	Val	Gly	Arg	Met	Asn	Lys	Ile	Val	Asp	180	185	190	
Ala	Glu	Gln	Leu	Gln	Val	Glu	Glu	Gly	Ser	Leu	Glu	Ile	Ile	Ala	Ser	195	200	205	

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Figure 1. Schematic diagram of the experimental setup.

(i) SEQUENCE CHARACTERISTICS:

- (v) FRAGMENT TYPE: internal

Ile Asp Glu Val His Met Leu Ser Thr Ala Ala Phe Asn Ala Leu Leu

003720"224960

130	135	140
Lys Thr Leu Glu Glu Pro Pro His Ala Lys Phe Ile Phe Ala Thr ⁻		
145	150	155 160
Thr Glu Ile Arg Lys Val Pro Val Thr Ile Leu Ser Arg Cys Gln Arg		
	165 170	175
Phe Asp Leu Arg Arg Val Glu Pro Asp Val Leu Val Lys His Phe Asp		
	180 185	190
Arg Ile Ser Ala Lys Glu Gly Ala Arg Ile Glu Met Asp Ala Leu Ala		
	195 200	205
Leu Ile Ala Arg Ala Ala Glu Gly Ser Val Arg Asp Gly Leu Ser Leu		
	210 215	220
Leu Asp Gln Ala Ile Val Gln Thr Glu Arg Gly Gln Thr Val Thr Ser		
225	230 235	240
Thr Val Val Arg Asp Met Leu Gly Leu Ala Asp Arg Ser Gln Thr Ile		
	245 250	255
Ala Leu Tyr Glu His Val Met Ala Gly Lys Thr Lys Asp Ala Leu Glu		
	260 265	270
Gly Phe Arg Ala Leu Trp Gly Phe Gly Ala Asp Pro Ala Val Val Met		
	275 280	285
Leu Asp Val Leu Asp His Cys His Ala Ser Ala Val		
	290 295	300

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 260 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met His Gln Val Phe Tyr Gln Lys Tyr Arg Pro Ile Asn Phe Lys Gln
1 5 10 15
Thr Leu Gly Gln Glu Ser Ile Arg Lys Ile Leu Val Asn Ala Ile Asn
20 25 30
Arg Asp Lys Leu Pro Asn Gly Tyr Ile Phe Ser Gly Glu Arg Gly Thr
35 40 45
Gly Lys Thr Thr Phe Ala Lys Ile Ile Ala Lys Ala Ile Asn Cys Leu
50 55 60

002120" 2724960

Gly	Arg	Leu	Ala	Gln	Ala	Tyr	Leu	Phe	Ser	Gly	Pro	Arg	Gly	Val	Gly	
		35					40					45				
Lys	Thr	Thr	Thr	Ala	Arg	Leu	Leu	Ala	Met	Ala	Val	Gly	Cys	Gln	Gly	
	50					55					60					
Glu	Asp	Pro	Pro	Cys	Gly	Val	Cys	Pro	His	Cys	Gln	Ala	Val	Gln	Arg	
65				70						75					80	
Gly	Ala	His	Pro	Asp	Val	Val	Asp	Ile	Asp	Ala	Ala	Ser	Asn	Asn	Ser	
			85					90						95		
Val	Glu	Asp	Val	Arg	Glu	Leu	Arg	Glu	Arg	Ile	His	Leu	Ala	Pro	Leu	
			100					105					110			
Ser	Ala	Pro	Arg	Lys	Val	Phe	Ile	Leu	Asp	Glu	Ala	His	Met	Leu	Ser	
		115					120						125			
Lys	Ser	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	Glu	Pro	Pro	Pro	
		130				135					140					
His	Val	Leu	Phe	Val	Phe	Ala	Thr	Thr	Glu	Pro	Glu	Arg	Met	Pro	Pro	
145					150					155					160	
Thr	Ile	Leu	Ser	Arg	Thr	Gln	His	Phe	Arg	Phe	Arg	Arg	Leu	Thr	Glu	
				165					170					175		
Glu	Glu	Ile	Ala	Phe	Lys	Leu	Arg	Arg	Ile	Leu	Glu	Ala	Val	Gly	Arg	
			180					185					190			
Glu	Ala	Glu	Glu	Glu	Ala	Leu	Leu	Leu	Leu	Ala	Arg	Leu	Ala	Asp	Gly	
		195				200						205				
Ala	Leu	Arg	Asp	Ala	Glu	Ser	Leu	Leu	Glu	Arg	Phe	Leu	Leu	Leu	Glu	
		210				215					220					
Gly	Pro	Leu	Thr	Arg	Lys	Glu	Val	Glu	Arg	Ala	Leu	Gly	Ser	Pro	Pro	
225					230					235					240	
Gly	Thr	Gly	Val	Ala	Glu	Ile	Ala	Ala	Ser	Leu	Ala	Arg	Gly	Lys	Thr	
				245					250					255		
Ala	Glu	Ala	Leu	Gly	Leu	Ala	Arg	Arg	Leu	Tyr	Gly	Glu	Gly	Tyr	Ala	
			260				265						270			
Pro	Arg	Ser	Leu	Val	Ser	Gly	Leu	Leu	Glu	Val	Phe	Arg	Glu	Gly	Leu	
		275					280					285				

Tyr

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: RNA (genomic)
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GUCCUGGAGG GAGAAAAAAA AAGCCUGAGC CCAAGGCCCC GCCCGGCCCC ACCUCCUGAA 60
GCGCCCGCAC CCCCggggccc UCCCGAGGAG GAGGUAGAGG C 101

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Val Leu Glu Gly Glu Lys Lys Ser Leu Ser Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CACGCNTACC TTTTCTCCGG NAC 23

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

008120"3F24960

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTGCTCNGGN GGCTCCTCNT CNGTC

25

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTGGGATCCG TGTTCTGGA TCTCGATGAA GAA

33

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GTGGGATCCA CGSCTSTCS GAGCAGAAG

29

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

008180" 31224960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GCGGGATCCT CAACGAGGAC CTCTCCATCT TCAA

34

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCGGGATCCT TGTCGTCSAG SGTSAGSGCG TCGTA

35

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGGAAGGACC AGCGCGTACT CCCCCTGCTC CTAGGTGTG

39

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"
- (iii) HYPOTHETICAL: NO

002130"31224960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTGTGGATCC TTCTTCTTSC CCATSGC

27

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CACCGATTCC AGTGGTGCCT AGGTGTG

27

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CAACACCTGG TGTTCAGGA GCCTGTGCTT

30

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CCAGAATCGT CTGCTGGTCG TAG

23

008780"8T224960

2025

(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

AGCACCTTGG AGGAGCTTC

19

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

CATGTCGTAC TGGGTGTAC

19

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

GTSGTSNNSG ACNNSGAGAC SACSGGG

27

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

- (iii) HYPOTHETICAL: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GAASCCSNNG TCGAASNNGG CGTTGTG

27

- (2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

- (iii) HYPOTHETICAL: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CGGGGATCCA CCTCAATCAC CTCGTGG

27

- (2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

- (iii) HYPOTHETICAL: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGGGGATCCG CCACCTTGCG GCTCCGGGTG

30

- (2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid

008780" 87224960

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GCGCTCTAGA CGAGTTCCCA AAGCGTGCGG T

31

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GCGGTCTAGA TCACCTGTAT CCAGA

25

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GCGGCGCATA TGGTGGTGGT CCTGGACCTG GAG

33

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

000130" 8724960

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGCGTCTAGA TCACCTGTAT CCAGA

25

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTSC TSGTSA AGACSCACTT

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

SAGSAGSGCG TTGAASGTGT G

21

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

00642218 081300

[illegible]

22

24

27

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TGCTGGCGTT CATCTTCAGG ATG

23

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CATCCTGAAG ATGAACGCCA GCA

23

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

AGGTTATCCA CAGGGGTCAT GTGCA

25

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

009642218 "001800

GTGTGTCATA TGAACATAAC GGTTCCTCAA

29

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCGCGAATTC TCCCTTGTGG AAGGCTTAG

29

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Arg Val Glu Leu Asp Tyr Asp Ala Leu Thr Leu Asp Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Phe Phe Ile Glu Ile Gln Asn His Gly Leu Ser Glu Gln Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids

00642218-001800

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Phe Phe Ile Glu Ile Gln Asn His
1 5

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Tyr Asp Ala Leu Thr Leu Asp Asp
1 5

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ala Met Gly Lys Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

00543218 001800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Phe Asn Lys Ser His Ser Ala Ala Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Val Val Xaa Asp Xaa Glu Thr Thr Gly
1 5

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

His Asn Ala Xaa Phe Asp Xaa Gly Phe
1 5

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Val Val Xaa Asp Xaa Glu Thr Thr Gly
1 5

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids

00542212.031200

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Val Leu Val Lys Thr His Leu
1 5

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

His Arg Ala Leu Tyr Asp
1 5

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

His Thr Phe Asn Ala Leu Leu
1 5

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

00642318061800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Asp Arg Tyr Phe Leu Glu Leu Ile Arg Thr Gly Arg Pro Asp Glu Glu
1 5 10 15
Ser Tyr Leu His Ala Ala Val Glu Leu Ala Glu Ala Arg Gly Leu Pro
20 25 30
Val Val

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Asp His Phe Tyr Leu Glu Leu Ile Arg Thr Gly Arg Ala Asp Glu Glu
1 5 10 15
Ser Tyr Leu His Phe Ala Leu Asp Val Ala Glu Gln Tyr Asp Leu Pro
20 25 30
Val Val

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Asp His Phe Tyr Leu Ala Leu Ser Arg Thr Gly Arg Pro Asn Glu Glu
1 5 10 15
Arg Tyr Ile Gln Ala Ala Leu Lys Leu Ala Glu Arg Cys Asp Leu Pro
20 25 30
Leu Val

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:

0034210"024960

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Asp Arg Phe Tyr Phe Glu Ile Met Arg His Asp Leu Pro Glu Glu Gln
 1 5 10 15
 Phe Ile Glu Asn Ser Tyr Ile Gln Ile Ala Ser Glu Leu Ser Ile Pro
 20 25 30
 Ile Val

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Asp Asp Phe Tyr Leu Glu Ile Met Arg His Gly Ile Leu Asp Gln Arg
 1 5 10 15
 Phe Ile Asp Glu Gln Val Ile Lys Met Ser Leu Glu Thr Gly Leu Lys
 20 25 30
 Ile Ile

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Asp Asp Tyr Tyr Leu Glu Ile Gln Asp His Gly Ser Val Glu Asp Arg
 1 5 10 15

0032218 081300

Leu Val Asn Ile Asn Leu Val Lys Ile Ala Gln Glu Leu Asp Ile Lys
 20 25 30

Ile Val

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Asp Asn Tyr Phe Leu Glu Leu Met Asp His Gly Leu Thr Ile Glu Arg
 1 5 10 15

Arg Val Arg Asp Gly Leu Leu Glu Ile Gly Arg Ala Leu Asn Ile Pro
 20 25 30

Pro Leu

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Asn Lys Arg Arg Ala Lys Asn Gly Glu Pro Pro Leu Asp Ile Ala Ala
 1 5 10 15

Ile Pro Leu Asp Asp Lys Lys Ser Phe Asp Met Leu Gln Arg Ser Glu
 20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp
 35 40 45

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

002130" 2224950

064218-000

(2) INFORMATION FOR SEQ ID NO:81:

(ii) MOLECULE TYPE: protein

Asn	Val	Arg	Met	Val	Arg	Glu	Gly	Lys	Pro	Arg	Val	Asp	Ile	Ala	Ala
1				5					10					15	
Ile	Pro	Leu	Asp	Asp	Pro	Glu	Ser	Phe	Glu	Leu	Leu	Lys	Arg	Ser	Glu
			20					25					30		
Thr	Thr	Ala	Val	Phe	Gln	Leu	Glu	Ser	Arg	Gly	Met	Lys	Asp		
		35					40					45			

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Cys Lys Lys Leu Leu Lys Glu Gln Gly Ile Lys Ile Asp Phe Asp Asp
1 5 10 15
Met Thr Phe Asp Asp Lys Lys Thr Tyr Gln Met Leu Cys Lys Gly Lys
20 25 30
Gly Val Gly Val Phe Gln Phe Glu Ser Ile Gly Met Lys Asp
35 40 45

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Leu Lys Ile Ile Lys Thr Gln His Lys Ile Ser Val Asp Phe Leu Ser
1 5 10 15
Leu Asp Met Asp Asp Pro Lys Val Tyr Lys Thr Ile Gln Ser Gly Asp
 20 25 30
Thr Val Gly Ile Phe Gln Ile Glu Ser Gly Met Phe Gln
 35 40 45

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Gln Glu Arg Lys Ala Leu Gln Ile Arg Ala Arg Thr Gly Ser Lys Lys
1 5 10 15
Leu Pro Asp Asp Val Lys Lys Thr His Lys Leu Leu Glu Ala Gly Asp
 20 25 30
Leu Glu Gly Ile Phe Gln Leu Glu Ser Gln Gly Met Lys Gln
 35 40 45

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

008490" 8244360

Ile Asp Asn Val Arg Ala Asn Arg Gly Ile Asp Leu Asp Leu Glu Ser
 1 5 10 15
 Val Pro Leu Asp Asp Lys Ala Thr Tyr Glu Leu Leu Gly Arg Gly Asp
 20 25 30
 Thr Leu Gly Val Phe Gln Leu Asp Gly Gly Pro Met Arg Asp
 35 40 45

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ATGGGCGGG AGCTCCGCTT CGCCACCTC CACCAGCACA CCCAGTTCTC CCTCCTGGAC 60
 GGGGCGCCGA AGCTTTCCGA CCTCCTCAAG TGGGTGGAGG AGACGACCCC CGAGGACCCC 120
 GCCTTGCCCA TGACCGACCA CGGCAACCTC TTCGGGGCCG TAGAGTTCTA CAAGAAGGCC 180
 GCCGAAATGG GCATCGAGCC CATCCTGGGT ACGAGGCCTT ACGTGGCGGC GGAAAGCCCC 240
 TTTGACCGCA AGCGGGGAAA GGGCCTAGAC GGGGGCTACT TTCACCTCAC CCTCCTCGCC 300
 AAGGACTTCA CGGGGTACCA GAACCTGGTG CGCCTGGCGA GCCGGGCTTA CCTGGAGGGG 360
 TTTTACGAAA AGCCCCGGAT TGACCGGGAG ATCCTGCGCG AGCGCCGAGG GCCTCATCGC 420
 CTCTCGGGGT GCCTCGGGGC GGAGATCCCC CAGTTCATCC TCCAGGACCG TCTGGACCTG 480
 GCCGAGGCCC GGCTCAACGA GGACCTCTCC ATCTTCAAGG ACCGCTTCTT CATTACATC 540
 CAGAACCACG GCCTCCCCGA GCAGAAAAAG GTCAACGAGG TCCTCAAGGA GTTCGCCCCGA 600
 AAGTACGGCC TGGGGATGGT GGCCACCAAC GACGGCCATT ACGGGAGGAA GGAGGCCCCG 660
 AGCGCCACG AGGTTTTCTT CGCCATCCAG TCCAAGAGCA CCCTGGACGA CCCCAGGGCC 720
 GTTGGCTTTC CCCTGCGGGA GTTCTACGTG AAGACCCCCG AGGAGACGTG CGGGCCGGTG 780
 TTCCCCGAGG AGGAGTGGGG GGACGAGCCC TTTGACAACA CCGTGGAGAT CGCCCGCATG 840
 TGCAACGTGG AGCTGCCCAT CGGGACAAGA TGGTCTACCC GAATCCCCCG CTTCCCCCTC 900
 CCCGAGGGAC CGGGGACCGA GGCCAAGTAC CTAATGGAGC TAACCTTCAA GGGGCCCCCTC 960
 CGCCGTTACC CGGACCGAAT CACCGAGGGT TTCTACCGGG AGGTTTTCCG CCTTTTGGGG 1020
 AAGCTTCCCC CCCACGGGCA CGGGGAGGCC TTGGCCGAGG CCTTGGCCCA GGTGGAGCGG 1080
 GAGGCTTGGG AGAGGCTCAT GAAGAGCCTC CCCCCCTTTG ACCGGGGTCC AAGGAGTTCC 1140
 A 1141

002120-01224960

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met Gly Arg Glu Leu Arg Phe Ala His Leu His Gln His Thr Gln Phe
1 5 10 15
Ser Leu Leu Asp Gly Ala Pro Lys Leu Ser Asp Leu Leu Lys Trp Val
20 25 30
Glu Glu Thr Thr Pro Glu Asp Pro Ala Leu Ala Met Thr Asp His Gly
35 40 45
Asn Leu Phe Gly Ala Val Glu Phe Tyr Lys Lys Ala Ala Glu Met Gly
50 55 60
Ile Glu Pro Ile Leu Gly Thr Arg Pro Tyr Val Ala Ala Glu Ser Pro
65 70 75 80
Phe Asp Arg Lys Arg Gly Lys Gly Leu Asp Gly Gly Tyr Phe His Leu
85 90 95
Thr Leu Leu Ala Lys Asp Phe Thr Gly Tyr Gln Asn Leu Val Arg Leu
100 105 110
Ala Ser Arg Ala Tyr Leu Glu Gly Phe Tyr Glu Lys Pro Arg Ile Asp
115 120 125
Arg Glu Ile Leu Arg Glu Arg Arg Gly Pro His Arg Leu Ser Gly Cys
130 135 140
Leu Gly Ala Glu Ile Pro Gln Phe Ile Leu Gln Asp Arg Leu Asp Leu
145 150 155 160
Phe Phe Ile Glu Ile Gln Asn His Gly Leu Ser Glu Gln Lys Ala Glu
165 170 175
Ala Arg Leu Asn Glu Asp Leu Ser Ile Phe Lys Asp Arg Phe Phe Ile
180 185 190
His Ile Gln Asn His Gly Leu Pro Glu Gln Lys Lys Val Asn Glu Val
195 200 205
Leu Lys Glu Phe Ala Arg Lys Tyr Gly Leu Gly Met Val Ala Thr Asn
210 215 220
Asp Gly His Tyr Gly Arg Lys Glu Ala Arg Ser Ala His Glu Val Phe
225 230 235 240
Leu Ala Ile Gln Ser Lys Ser Thr Leu Asp Asp Pro Gly Ala Val Gly
245 250 255

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Phe Pro Leu Arg Glu Phe Tyr Val Lys Thr Pro Glu Glu Thr Cys Gly
 260 265 270
 Pro Val Phe Pro Glu Glu Glu Trp Gly Asp Glu Pro Phe Asp Asn Thr
 275 280 285
 Val Glu Ile Ala Arg Met Cys Asn Val Glu Leu Pro Ile Gly Thr Arg
 290 295 300
 Trp Ser Thr Arg Ile Pro Arg Phe Pro Leu Pro Glu Gly Pro Gly Thr
 305 310 315 320
 Glu Ala Lys Tyr Leu Met Glu Leu Thr Phe Lys Gly Pro Leu Arg Arg
 325 330 335
 Tyr Pro Asp Arg Ile Thr Glu Gly Phe Tyr Arg Glu Val Phe Arg Leu
 340 345 350
 Leu Gly Lys Leu Pro Pro His Gly His Gly Glu Ala Leu Ala Glu Ala
 355 360 365
 Leu Ala Gln Val Glu Arg Glu Ala Trp Glu Arg Leu Met Lys Ser Leu
 370 375 380
 Pro Pro Phe Asp Arg Gly Pro Arg Ser Ser
 385 390

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu Glu
 1 5 10 15
 Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu Gly
 20 25 30
 Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly Leu
 35 40 45
 Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg Arg
 50 55 60
 Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala Arg
 65 70 75 80
 Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala Pro
 85 90 95
 Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp Ala
 100 105 110

008F80"21224360

Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg Pro
 115 120 125
 Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp Ser
 130 135 140
 Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly Leu
 145 150 155 160
 Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His Arg
 165 170 175
 Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val Tyr
 180 185 190
 Tyr Met Leu Thr Ser Gly
 195

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Pro Trp Pro Gln Asp Val Val Val Phe Asp Leu Glu Thr Thr Gly Phe
 1 5 10 15
 Ser Pro Ala Ser Ala Ala Ile Val Glu Ile Gly Ala Val Arg Ile Val
 20 25 30
 Gly Gly Gln Ile Asp Glu Thr Leu Lys Phe Glu Thr Leu Val Arg Pro
 35 40 45
 Thr Arg Pro Asp Gly Ser Met Leu Ser Ile Pro Trp Gln Ala Gln Arg
 50 55 60
 Val His Gly Ile Ser Asp Glu Met Val Arg Arg Ala Pro Ala Xaa Lys
 65 70 75 80
 Asp Val Leu Pro Asp Phe Phe Asp Phe Val Asp Gly Ser Ala Val Val
 85 90 95
 Ala His Asn Val Ser Phe Asp Gly Gly Phe Met Arg Ala Gly Ala Glu
 100 105 110
 Arg Leu Gly Leu Ser Trp Ala Pro Glu Arg Glu Leu Cys Thr Met Gln
 115 120 125
 Leu Ser Arg Arg Ala Phe Pro Arg Glu Arg Thr His Asn Leu Thr Val
 130 135 140
 Leu Ala Glu Arg Leu Gly Leu Glu Phe Ala Pro Gly Gly Arg His Arg
 145 150 155 160

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Ser Tyr Gly Asp Val Gln Val Thr Ala Gln Ala Tyr Leu Arg Leu Leu
165 170 175
Glu Leu Leu Gly Glu Arg
180

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

His Gly Ile Lys Met Ile Tyr Gly Met Glu Ala Asn Leu Val Asp Asp
1 5 10 15
Gly Val Pro Ile Ala Tyr Asn Ala Ala His Arg Leu Leu Glu Glu Glu
20 25 30
Thr Tyr Val Val Phe Asp Val Glu Thr Thr Gly Leu Ser Ala Val Tyr
35 40 45
Asp Thr Ile Ile Glu Leu Ala Ala Val Lys Val Lys Gly Gly Glu Ile
50 55 60
Ile Asp Lys Phe Glu Ala Phe Ala Asn Pro His Arg Pro Leu Ser Ala
65 70 75 80
Thr Ile Ile Glu Leu Thr Gly Ile Thr Asp Asp Met Leu Gln Asp Ala
85 90 95
Pro Asp Val Val Asp Val Ile Arg Asp Phe Arg Glu Trp Ile Gly Asp
100 105 110
Asp Ile Leu Val Ala His Asn Ala Ser Phe Asp Met Gly Phe Leu Asn
115 120 125
Val Ala Tyr Lys Lys Leu Leu Glu Val Glu Lys Ala Lys Asn Pro Val
130 135 140
Ile Asp Thr Leu Glu Leu Gly Arg Phe Leu Tyr Pro Glu Phe Lys Asn
145 150 155 160
His Arg Leu Asn Thr Leu Cys Lys Lys Phe Asp Ile Glu Leu Thr Gln
165 170 175
His His Arg Ala Ile Tyr Asp Thr Glu Ala Thr Ala Tyr Leu Leu Leu
180 185 190
Lys Met Leu Lys Asp Ala Ala Glu Lys
195 200

(2) INFORMATION FOR SEQ ID NO:91:

003423-03100

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 188 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Met	Ile	Asn	Pro	Asn	Arg	Gln	Ile	Val	Leu	Asp	Thr	Glu	Thr	Thr	Gly	1	5	10	15
Met	Asn	Gln	Leu	Gly	Ala	His	Tyr	Glu	Gly	His	Cys	Ile	Ile	Glu	Ile	20	25	30	
Gly	Ala	Val	Glu	Leu	Ile	Asn	Arg	Arg	Tyr	Thr	Gly	Asn	Asn	Xaa	His	35	40	45	
Ile	Tyr	Ile	Lys	Pro	Asp	Arg	Pro	Xaa	Asp	Pro	Asp	Ala	Ile	Lys	Val	50	55	60	
His	Gly	Ile	Thr	Asp	Glu	Met	Leu	Ala	Asp	Lys	Pro	Glu	Phe	Lys	Glu	65	70	75	80
Val	Ala	Gln	Asp	Phe	Leu	Asp	Tyr	Ile	Asn	Gly	Ala	Glu	Leu	Leu	Ile	85	90	95	
His	Asn	Ala	Pro	Phe	Asp	Val	Gly	Phe	Met	Asp	Tyr	Glu	Phe	Arg	Lys	100	105	110	
Leu	Asn	Leu	Asn	Val	Lys	Thr	Asp	Asp	Ile	Cys	Leu	Val	Thr	Asp	Thr	115	120	125	
Leu	Gln	Met	Ala	Arg	Gln	Met	Tyr	Pro	Gly	Lys	Arg	Asn	Asn	Leu	Asp	130	135	140	
Ala	Leu	Cys	Asp	Arg	Leu	Gly	Ile	Asp	Asn	Ser	Lys	Arg	Thr	Leu	His	145	150	155	160
Gly	Ala	Leu	Leu	Asp	Ala	Glu	Ile	Leu	Ala	Asp	Val	Tyr	Leu	Met	Met	165	170	175	
Thr	Gly	Gly	Gln	Thr	Asn	Leu	Phe	Asp	Glu	Glu	Glu					180	185		

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 189 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met 1	Ser	Thr	Ala	Ile 5	Thr	Arg	Gln	Ile	Val 10	Leu	Asp	Thr	Glu	Thr 15	Thr
Gly	Met	Asn	Gln 20	Ile	Gly	Ala	His	Ser 25	Glu	Gly	His	Lys	Ile 30	Ile	Glu
Ile	Gly	Ala 35	Val	Glu	Val	Val	Asn 40	Arg	Arg	Leu	Thr	Gly 45	Asn	Asn	Phe
His 50	Val	Tyr	Leu	Lys	Asp	Arg 55	Leu	Val	Asp	Pro	Glu 60	Ala	Phe	Gly	Val
His 65	Gly	Ile	Ala	Val	Asp 70	Phe	Leu	Leu	Asp 75	Lys	Pro	Thr	Phe	Ala	Glu 80
Val	Ala	Val	Glu	Phe 85	Met	Asp	Tyr	Ile	Arg 90	Gly	Ala	Glu	Leu	Val 95	Ile
His	Asn	Ala	Ala 100	Phe	Asp	Ile	Gly	Phe 105	Met	Asp	Tyr	Glu	Phe 110	Ser	Leu
Leu	Lys	Arg 115	Asp	Ile	Ala	Lys	Thr 120	Asn	Thr	Phe	Cys	Lys 125	Val	Thr	Asp
Ser 130	Leu	Ala	Val	Ala	Arg	Lys 135	Met	Phe	Pro	Gly	Lys 140	Arg	Asn	Ser	Leu
Asp 145	Ala	Leu	Cys	Ala	Arg 150	Tyr	Glu	Ile	Asp	Asn 155	Ser	Lys	Arg	Thr	Leu 160
His	Gly	Ala	Leu	Leu 165	Asp	Ala	Gln	Ile	Leu 170	Ala	Glu	Val	Tyr	Leu 175	Ala
Met	Thr	Gly	Gly 180	Gln	Thr	Ser	Met	Ala 185	Phe	Ala	Met	Glu			

(2) INFORMATION FOR SEQ ID NO:93:

(ii) MOLECULE TYPE: protein

Asn	Leu	Glu	Tyr	Leu	Lys	Ala	Cys	Gly	Leu	Asn	Phe	Ile	Glu	Thr	Ser
1				5					10					15	
Glu	Asn	Leu	Ile	Thr	Leu	Lys	Asn	Leu	Lys	Thr	Pro	Leu	Lys	Asp	Glu
			20					25					30		
Val	Phe	Ser	Phe	Ile	Asp	Leu	Glu	Thr	Thr	Gly	Ser	Cys	Pro	Ile	Lys
		35					40					45			
His	Glu	Ile	Leu	Glu	Ile	Gly	Ala	Val	Gln	Val	Lys	Gly	Gly	Glu	Ile
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Met Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu
 1 5 10 15
 Glu Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu
 20 25 30
 Gly Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly
 35 40 45
 Leu Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg
 50 55 60
 Arg Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala
 65 70 75 80
 Arg Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala
 85 90 95
 Pro Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp
 100 105 110
 Ala Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg
 115 120 125
 Pro Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp
 130 135 140
 Ser Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly
 145 150 155 160
 Leu Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His
 165 170 175
 Arg Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val
 180 185 190
 Tyr Tyr Met Leu Thr Ser Gly Arg Pro Arg Thr Leu Trp Glu Leu Gly
 195 200 205
 Arg Glx
 210

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Met	Leu	Glu	Ala	Ser	Trp	Glu	Lys	Val	Gln	Ser	Ser	Leu	Lys	Gln	Asn	1	5	10	15
Leu	Ser	Lys	Pro	Ser	Tyr	Glu	Thr	Trp	Ile	Arg	Pro	Thr	Glu	Phe	Ser	20	25	30	
Gly	Phe	Lys	Asn	Gly	Glu	Leu	Thr	Leu	Ile	Ala	Pro	Asn	Ser	Phe	Ser	35	40	45	
Ser	Ala	Trp	Leu	Lys	Asn	Asn	Tyr	Ser	Gln	Thr	Ile	Gln	Glu	Thr	Ala	50	55	60	
Glu	Glu	Ile	Phe	Gly	Glu	Pro	Val	Thr	Val	His	Val	Lys	Val	Lys	Ala	65	70	75	80
Asn	Ala	Glu	Ser	Ser	Asp	Glu	His	Tyr	Ser	Ser	Ala	Pro	Ile	Thr	Pro	85	90	95	
Pro	Leu	Glu	Ala	Ser	Pro	Gly	Ser	Val	Asp	Ser	Ser	Gly	Ser	Ser	Leu	100	105	110	
Arg	Leu	Ser	Lys	Lys	Thr	Leu	Pro	Leu	Leu	Asn	Leu	Arg	Tyr	Val	Phe	115	120	125	
Asn	Arg	Phe	Val	Val	Gly	Pro	Asn	Ser	Arg	Met	Ala	His	Ala	Ala	Ala	130	135	140	
Met	Ala	Val	Ala	Glu	Ser	Pro	Gly	Arg	Glu	Phe	Asn	Pro	Leu	Phe	Ile	145	150	155	160
Cys	Gly	Gly	Val	Gly	Leu	Gly	Lys	Thr	His	Leu	Met	Gln	Ala	Ile	Gly	165	170	175	
His	Tyr	Arg	Leu	Glu	Ile	Asp	Pro	Gly	Ala	Lys	Val	Ser	Tyr	Val	Ser	180	185	190	
Thr	Glu	Thr	Phe	Thr	Asn	Asp	Leu	Ile	Leu	Ala	Ile	Arg	Gln	Asp	Arg	195	200	205	
Met	Gln	Ala	Phe	Arg	Asp	Arg	Tyr	Arg	Ala	Ala	Asp	Leu	Ile	Leu	Val	210	215	220	
Asp	Asp	Ile	Gln	Phe	Ile	Glu	Gly	Lys	Glu	Tyr	Thr	Gln	Glu	Glu	Phe	225	230	235	240
Phe	His	Thr	Phe	Asn	Ala	Leu	His	Asp	Ala	Gly	Ser	Gln	Ile	Val	Leu	245	250	255	
Ala	Ser	Asp	Arg	Pro	Pro	Ser	Gln	Ile	Pro	Arg	Leu	Gln	Glu	Arg	Leu	260	265	270	
Met	Ser	Arg	Phe	Ser	Met	Gly	Leu	Ile	Ala	Asp	Val	Gln	Ala	Pro	Asp				

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275							280				285				
Leu	Glu	Thr	Arg	Met	Ala	Ile	Leu	Gln	Lys	Lys	Ala	Glu	His	Glu	Arg
	290					295					300				
Val	Gly	Leu	Pro	Arg	Asp	Leu	Ile	Gln	Phe	Ile	Ala	Gly	Arg	Phe	Thr
305					310					315					320
Ser	Asn	Ile	Arg	Glu	Leu	Glu	Gly	Ala	Leu	Thr	Arg	Ala	Ile	Ala	Phe
				325					330					335	
Ala	Ser	Ile	Thr	Gly	Leu	Pro	Met	Thr	Val	Asp	Ser	Ile	Ala	Pro	Met
			340				345						350		
Leu	Asp	Pro	Asn	Gly	Gln	Gly	Val	Glu	Val	Thr	Pro	Lys	Gln	Val	Leu
		355					360					365			
Asp	Lys	Val	Ala	Glu	Val	Phe	Lys	Val	Thr	Pro	Asp	Glu	Met	Arg	Ser
	370					375					380				
Ala	Ser	Arg	Arg	Arg	Pro	Val	Ser	Gln	Ala	Arg	Gln	Val	Gly	Met	Tyr
385					390					395					400
Leu	Met	Arg	Gln	Gly	Thr	Asn	Leu	Ser	Leu	Pro	Arg	Ile	Gly	Asp	Thr
				405					410					415	
Phe	Gly	Gly	Lys	Asp	His	Thr	Thr	Val	Met	Tyr	Ala	Ile	Glu	Gln	Val
			420				425						430		
Glu	Lys	Lys	Leu	Ser	Ser	Asp	Pro	Gln	Ile	Ala	Ser	Gln	Val	Gln	Lys
		435					440					445			
Ile	Arg	Asp	Leu	Leu	Gln	Ile	Asp	Ser	Arg	Arg	Lys	Arg			
	450					455					460				

(2) INFORMATION FOR SEQ ID NO:97:

(ii) MOLECULE TYPE: protein

Met Val Ser Cys Glu Asn Leu Trp Gln Gln Ala Leu Ala Ile Leu Ala
1 5 10 15

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65						70						75						80
Asp	Gly	Leu	Glu	Pro	His	Ser	Leu	Ile	Gly	Gln	Glu	Ser	Ser	Leu	Pro			
				85					90					95				
Met	Glu	Thr	Thr	Pro	Lys	Asn	Ala	Thr	Ala	Leu	Asn	Gly	Lys	Tyr	Thr			
			100					105					110					
Phe	Ser	Arg	Phe	Val	Val	Gly	Pro	Thr	Asn	Arg	Met	Ala	His	Ala	Ala			
		115					120					125						
Ser	Leu	Ala	Val	Ala	Glu	Ser	Pro	Gly	Arg	Glu	Phe	Asn	Pro	Leu	Phe			
		130					135					140						
Leu	Cys	Gly	Gly	Val	Gly	Leu	Gly	Lys	Thr	His	Leu	Met	Gln	Ala	Ile			
145					150					155					160			
Ala	His	Tyr	Arg	Leu	Glu	Met	Tyr	Pro	Asn	Ala	Lys	Val	Tyr	Tyr	Val			
				165					170					175				
Ser	Thr	Glu	Arg	Phe	Thr	Asn	Asp	Leu	Ile	Thr	Ala	Ile	Arg	Gln	Asp			
			180					185					190					
Asn	Met	Glu	Asp	Phe	Arg	Ser	Tyr	Tyr	Arg	Ser	Ala	Asp	Phe	Leu	Leu			
		195					200					205						
Ile	Asp	Asp	Ile	Gln	Phe	Ile	Lys	Gly	Lys	Glu	Tyr	Thr	Gln	Glu	Glu			
	210					215					220							
Phe	Phe	His	Thr	Phe	Asn	Ser	Leu	His	Glu	Ala	Gly	Lys	Gln	Val	Val			
225					230					235					240			
Val	Ala	Ser	Asp	Arg	Ala	Pro	Gln	Arg	Ile	Pro	Gly	Leu	Gln	Asp	Arg			
				245					250					255				
Leu	Ile	Ser	Arg	Phe	Ser	Met	Gly	Leu	Ile	Ala	Asp	Ile	Gln	Val	Pro			
			260					265					270					
Asp	Leu	Glu	Thr	Arg	Met	Ala	Ile	Leu	Gln	Lys	Lys	Ala	Glu	Tyr	Asp			
		275					280					285						
Arg	Ile	Arg	Leu	Pro	Lys	Glu	Val	Ile	Glu	Tyr	Ile	Ala	Ser	His	Tyr			
	290					295					300							
Thr	Ser	Asn	Ile	Arg	Glu	Leu	Glu	Gly	Ala	Leu	Ile	Arg	Ala	Ile	Ala			
305					310					315					320			
Tyr	Thr	Ser	Leu	Ser	Asn	Val	Ala	Met	Thr	Val	Glu	Asn	Ile	Ala	Pro			
				325					330					335				
Val	Leu	Asn	Pro	Pro	Val	Glu	Lys	Val	Ala	Ala	Ala	Pro	Glu	Thr	Ile			
			340					345					350					
Ile	Thr	Ile	Val	Ala	Gln	His	Tyr	Gln	Leu	Lys	Val	Glu	Glu	Leu	Leu			
		355					360					365						
Ser	Asn	Ser	Arg	Arg	Arg	Glu	Val	Ser	Leu	Ala	Arg	Gln	Val	Gly	Met			
		370				375					380							
Tyr	Leu	Met	Arg	Gln	His	Thr	Asp	Leu	Ser	Leu	Pro	Arg	Ile	Gly	Glu			
385					390					395					400			
Ala	Phe	Gly	Gly	Lys	Asp	His	Thr	Thr	Val	Met	Tyr	Ser	Cys	Asp	Lys			

415

Ser Leu Ser His Arg Ile Asn Ile Ala Gly Gln Ala Pro Glu Ser
435 440 445

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Met 1	Glu	Asn	Ile	Leu 5	Asp	Leu	Trp	Asn	Gln 10	Ala	Leu	Ala	Gln	Ile 15	Glu
Lys	Lys	Leu	Ser 20	Lys	Pro	Ser	Phe	Glu 25	Thr	Trp	Met	Lys	Ser 30	Thr	Lys
Ala	His	Ser 35	Leu	Gln	Gly	Asp	Thr 40	Leu	Thr	Ile	Thr 45	Pro	Asn	Glu	
Phe	Ala 50	Arg	Asp	Trp	Leu	Glu 55	Ser	Arg	Tyr	Leu	His 60	Leu	Ile	Ala	Asp
Thr 65	Ile	Tyr	Glu	Leu	Thr 70	Gly	Glu	Glu	Leu	Ser 75	Ile	Lys	Phe	Val	Ile 80
Pro	Gln	Asn	Gln	Asp 85	Val	Glu	Asp	Phe	Met 90	Pro	Lys	Pro	Gln	Val 95	Lys
Lys	Ala	Val	Lys 100	Glu	Asp	Thr	Ser	Asp 105	Phe	Pro	Gln	Asn	Met 110	Leu	Asn
Pro	Lys	Tyr 115	Thr	Phe	Asp	Thr	Phe 120	Val	Ile	Gly	Ser	Gly 125	Asn	Arg	Phe
Ala	His 130	Ala	Ala	Ser	Leu	Ala 135	Val	Ala	Glu	Ala	Pro 140	Ala	Lys	Ala	Tyr
Asn 145	Pro	Leu	Phe	Ile	Tyr 150	Gly	Gly	Val	Gly	Leu 155	Gly	Lys	Thr	His	Leu 160
Met	His	Ala	Ile	Gly 165	His	Tyr	Val	Ile	Asp 170	His	Asn	Pro	Ser	Ala 175	Lys
Val	Val	Tyr	Leu 180	Ser	Ser	Glu	Lys	Phe 185	Thr	Asn	Glu	Phe	Ile 190	Asn	Ser
Ile	Arg	Asp 195	Asn	Lys	Ala	Val	Asp 200	Phe	Arg	Asn	Arg	Tyr 205	Arg	Asn	Val
Asp	Val	Leu	Leu	Ile	Asp	Asp	Ile	Gln	Phe	Leu	Ala	Gly	Lys	Glu	Gln

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003130" 322450

210	215	220
Thr Gln Glu Glu Phe Phe His Thr Phe Asn Thr Leu His Glu Glu Ser 225 230 235 240		
Lys Gln Ile Val Ile Ser Ser Asp Arg Pro Pro Lys Glu Ile Pro Thr 245 250 255		
Leu Glu Asp Arg Leu Arg Ser Arg Phe Glu Trp Gly Leu Ile Thr Asp 260 265 270		
Ile Thr Pro Pro Asp Leu Glu Thr Arg Ile Ala Ile Leu Arg Lys Lys 275 280 285		
Ala Lys Ala Glu Gly Leu Asp Ile Pro Asn Glu Val Met Leu Tyr Ile 290 295 300		
Ala Asn Gln Ile Asp Ser Asn Ile Arg Glu Leu Glu Gly Ala Leu Ile 305 310 315 320		
Arg Val Val Ala Tyr Ser Ser Leu Ile Asn Lys Asp Ile Asn Ala Asp 325 330 335		
Leu Ala Ala Glu Ala Leu Lys Asp Ile Ile Pro Ser Ser Lys Pro Lys 340 345 350		
Val Ile Thr Ile Lys Glu Ile Gln Arg Val Val Gly Gln Gln Phe Asn 355 360 365		
Ile Lys Leu Glu Asp Phe Lys Ala Lys Lys Arg Thr Lys Ser Val Ala 370 375 380		
Phe Pro Arg Gln Ile Ala Met Tyr Leu Ser Arg Glu Met Thr Asp Ser 385 390 395 400		
Ser Leu Pro Lys Ile Gly Glu Glu Phe Gly Gly Arg Asp His Thr Thr 405 410 415		
Val Ile His Ala His Glu Lys Ile Ser Lys Leu Leu Ala Asp Asp Glu 420 425 430		
Gln Leu Gln Gln His Val Lys Glu Ile Lys Glu Gln Leu Lys 435 440 445		

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Met Thr Asp Asp Pro Gly Ser Gly Phe Thr Thr Val Trp Asn Ala Val
1 5 10 15

Val Ser Glu Leu Asn Gly Asp Pro Lys Val Asp Asp Gly Pro Ser Ser

008180" 81224960

20					25					30					
Asp	Ala	Asn	Leu	Ser	Ala	Pro	Leu	Thr	Pro	Gln	Gln	Arg	Ala	Trp	Leu
	35						40					45			
Asn	Leu	Val	Gln	Pro	Leu	Thr	Ile	Val	Glu	Gly	Phe	Ala	Leu	Leu	Ser
	50					55					60				
Val	Pro	Ser	Ser	Phe	Val	Gln	Asn	Glu	Ile	Glu	Arg	His	Leu	Arg	Ala
65				70						75					80
Pro	Ile	Thr	Asp	Ala	Leu	Ser	Arg	Arg	Leu	Gly	His	Gln	Ile	Gln	Leu
				85					90					95	
Gly	Val	Arg	Ile	Ala	Pro	Pro	Ala	Thr	Asp	Glu	Ala	Asp	Asp	Thr	Thr
			100					105					110		
Val	Pro	Pro	Ser	Glu	Asn	Pro	Ala	Thr	Thr	Ser	Pro	Asp	Thr	Thr	Thr
			115				120					125			
Asp	Asn	Asp	Glu	Ile	Asp	Asp	Ser	Ala	Ala	Ala	Arg	Gly	Asp	Asn	Gln
	130					135						140			
His	Ser	Trp	Pro	Ser	Tyr	Phe	Thr	Glu	Arg	Pro	His	Asn	Thr	Asp	Ser
145				150						155					160
Ala	Thr	Ala	Gly	Val	Thr	Ser	Leu	Asn	Arg	Arg	Tyr	Thr	Phe	Asp	Thr
				165					170					175	
Phe	Val	Ile	Gly	Ala	Ser	Asn	Arg	Phe	Ala	His	Ala	Ala	Ala	Leu	Ala
			180					185					190		
Ile	Ala	Glu	Ala	Pro	Ala	Arg	Ala	Tyr	Asn	Pro	Leu	Phe	Ile	Trp	Gly
		195					200					205			
Glu	Ser	Gly	Leu	Gly	Lys	Thr	His	Leu	Leu	His	Ala	Ala	Gly	Asn	Tyr
	210					215					220				
Ala	Gln	Arg	Leu	Phe	Pro	Gly	Met	Arg	Val	Lys	Tyr	Val	Ser	Thr	Glu
225				230						235					240
Glu	Phe	Thr	Asn	Asp	Phe	Ile	Asn	Ser	Leu	Arg	Asp	Asp	Arg	Lys	Val
				245					250					255	
Ala	Phe	Lys	Arg	Ser	Tyr	Arg	Asp	Val	Asp	Val	Leu	Leu	Val	Asp	Asp
			260					265					270		
Ile	Gln	Phe	Ile	Glu	Gly	Lys	Glu	Gly	Ile	Gln	Glu	Glu	Phe	Phe	His
		275					280					285			
Thr	Phe	Asn	Thr	Leu	His	Asn	Ala	Asn	Lys	Gln	Ile	Val	Ile	Ser	Ser
	290					295					300				
Asp	Arg	Pro	Pro	Lys	Gln	Leu	Ala	Thr	Leu	Glu	Asp	Arg	Leu	Arg	Thr
305				310						315					320
Arg	Phe	Glu	Trp	Gly	Leu	Ile	Thr	Asp	Val	Gln	Pro	Pro	Glu	Leu	Glu
				325					330					335	
Thr	Arg	Ile	Ala	Ile	Leu	Arg	Lys	Lys	Ala	Gln	Met	Glu	Arg	Leu	Ala
			340					345					350		
Val	Pro	Asp	Asp	Val	Leu	Glu	Leu	Ile	Ala	Ser	Ser	Ile	Glu	Arg	Asn

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355	360	365
Ile Arg Glu Leu Glu Gly Ala Leu Ile Arg Val Thr Ala Phe Ala Ser		
370	375	380
Leu Asn Lys Thr Pro Ile Asp Lys Ala Leu Ala Glu Ile Val Leu Arg		
385	390	395 400
Asp Leu Ile Ala Asp Ala Asn Thr Met Gln Ile Ser Ala Ala Thr Ile		
405	410	415
Met Ala Ala Thr Ala Glu Tyr Phe Asp Thr Thr Val Glu Glu Leu Arg		
420	425	430
Gly Pro Gly Lys Thr Arg Ala Leu Ala Gln Ser Arg Gln Ile Ala Met		
435	440	445
Tyr Leu Cys Arg Glu Leu Thr Asp Leu Ser Leu Pro Lys Ile Gly Gln		
450	455	460
Ala Phe Gly Arg Asp His Thr Thr Val Met Tyr Ala Gln Arg Lys Ile		
465	470	475 480
Leu Ser Glu Met Ala Glu Arg Arg Glu Val Phe Asp His Val Lys Glu		
485	490	495
Leu Thr Thr Arg Ile Arg Gln Arg Ser Lys Arg		
500	505	

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg	
1 5 10 15	
Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro	
20 25 30	
Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe	
35 40 45	
Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly	
50 55 60	
Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val	
65 70 75 80	
Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro	
85 90 95	
Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly	

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100					105					110					
Pro	Thr	Thr	Pro	Trp	Pro	His	Gly	Gly	Ala	Val	Ala	Val	Ala	Glu	Ser
		115					120					125			
Pro	Gly	Arg	Ala	Tyr	Asn	Pro	Leu	Phe	Ile	Tyr	Gly	Gly	Arg	Gly	Leu
	130					135					140				
Gly	Lys	Thr	Tyr	Leu	Met	His	Ala	Val	Gly	Pro	Leu	Arg	Ala	Lys	Arg
145					150					155					160
Phe	Pro	His	Met	Arg	Leu	Glu	Tyr	Val	Ser	Thr	Glu	Thr	Phe	Thr	Asn
			165						170					175	
Glu	Leu	Ile	Asn	Arg	Pro	Ser	Ala	Arg	Asp	Arg	Met	Thr	Glu	Phe	Arg
			180					185					190		
Glu	Arg	Tyr	Arg	Ser	Val	Asp	Leu	Leu	Val	Asp	Asp	Val	Gln	Phe	
		195					200				205				
Ile	Ala	Gly	Lys	Glu	Arg	Thr	Gln	Glu	Glu	Phe	Phe	His	Thr	Phe	Asn
	210					215					220				
Ala	Leu	Tyr	Glu	Ala	His	Lys	Gln	Ile	Ile	Leu	Ser	Ser	Asp	Arg	Pro
225					230					235					240
Pro	Lys	Asp	Ile	Leu	Thr	Leu	Glu	Ala	Arg	Leu	Arg	Ser	Arg	Phe	Glu
			245						250					255	
Trp	Gly	Leu	Ile	Thr	Asp	Asn	Pro	Ala	Pro	Asp	Leu	Glu	Thr	Arg	Ile
		260						265					270		
Ala	Ile	Leu	Lys	Met	Asn	Ala	Ser	Ser	Gly	Pro	Glu	Asp	Pro	Glu	Asp
	275					280						285			
Ala	Leu	Glu	Tyr	Ile	Ala	Arg	Gln	Val	Thr	Ser	Asn	Ile	Arg	Glu	Trp
	290					295					300				
Glu	Gly	Ala	Leu	Met	Arg	Ala	Ser	Pro	Phe	Ala	Ser	Leu	Asn	Gly	Val
305					310					315					320
Glu	Leu	Thr	Arg	Ala	Val	Ala	Ala	Lys	Ala	Leu	Arg	His	Leu	Arg	Pro
			325						330					335	
Arg	Glu	Leu	Glu	Ala	Asp	Pro	Leu	Glu	Ile	Ile	Arg	Lys	Ala	Ala	Gly
		340						345					350		
Pro	Val	Arg	Pro	Glu	Thr	Pro	Gly	Gly	Ala	His	Gly	Glu	Arg	Arg	Lys
		355					360					365			
Lys	Glu	Val	Val	Leu	Pro	Arg	Gln	Leu	Ala	Met	Tyr	Leu	Val	Arg	Glu
	370					375					380				
Leu	Thr	Pro	Ala	Ser	Leu	Pro	Glu	Ile	Gly	Gln	Leu	Phe	Gly	Gly	Arg
385					390					395					400
Asp	His	Thr	Thr	Val	Arg	Tyr	Ala	Ile	Gln	Lys	Val	Gln	Glu	Leu	Ala
			405						410				415		
Gly	Lys	Pro	Asp	Arg	Glu	Val	Gln	Gly	Leu	Leu	Arg	Thr	Leu	Arg	Glu
		420						425					430		
Ala	Cys	Thr	Asp	Pro	Val	Asp	Asn	Leu	Trp	Ile	Thr	Cys	Gly		

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245										250					255				
Leu	Leu	Glu	Gly	Asn	Gln	Gln	Ile	Ile	Leu	Thr	Ser	Asp	Arg	Tyr	Pro				
			260					265					270						
Lys	Glu	Ile	Asn	Gly	Val	Glu	Asp	Arg	Leu	Lys	Ser	Arg	Phe	Gly	Trp				
		275					280					285							
Gly	Leu	Thr	Val	Ala	Ile	Glu	Pro	Pro	Glu	Leu	Glu	Thr	Arg	Val	Ala				
	290					295					300								
Ile	Leu	Met	Lys	Lys	Ala	Asp	Glu	Asn	Asp	Ile	Arg	Leu	Pro	Gly	Glu				
305					310				315						320				
Val	Ala	Phe	Phe	Ile	Ala	Lys	Arg	Leu	Arg	Ser	Asn	Val	Arg	Glu	Leu				
				325				330						335					
Glu	Gly	Ala	Leu	Asn	Arg	Val	Ile	Ala	Asn	Ala	Asn	Phe	Thr	Gly	Arg				
			340					345					350						
Ala	Ile	Thr	Ile	Asp	Phe	Val	Arg	Glu	Ala	Leu	Arg	Asp	Leu	Leu	Ala				
		355					360					365							
Leu	Gln	Glu	Lys	Leu	Val	Thr	Ile	Asp	Asn	Ile	Gln	Lys	Thr	Val	Ala				
	370					375					380								
Glu	Tyr	Tyr	Lys	Ile	Lys	Val	Ala	Asp	Leu	Leu	Ser	Lys	Arg	Arg	Ser				
385					390				395						400				
Arg	Ser	Val	Ala	Arg	Pro	Arg	Gln	Met	Ala	Met	Ala	Leu	Ala	Lys	Glu				
				405				410						415					
Leu	Thr	Asn	His	Ser	Leu	Pro	Glu	Ile	Gly	Asp	Ala	Phe	Gly	Gly	Arg				
			420					425					430						
Asp	His	Thr	Thr	Val	Leu	His	Ala	Cys	Arg	Lys	Ile	Glu	Gln	Leu	Arg				
		435					440					445							
Glu	Glu	Ser	His	Asp	Ile	Lys	Glu	Asp	Phe	Ser	Asn	Leu	Ile	Arg	Thr				
	450					455					460								
Leu	Ser	Ser																	
	465																		

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Met	Lys	Glu	Arg	Ile	Leu	Gln	Glu	Ile	Lys	Thr	Arg	Val	Asn	Arg	Lys
1				5				10					15		
Ser	Trp	Glu	Leu	Trp	Phe	Ser	Ser	Phe	Asp	Val	Lys	Ser	Ile	Glu	Gly

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20					25					30					
Asn	Lys	Val	Val	Phe	Ser	Val	Gly	Asn	Leu	Phe	Ile	Lys	Glu	Trp	Leu
	35						40					45			
Glu	Lys	Lys	Tyr	Tyr	Ser	Val	Leu	Ser	Lys	Ala	Val	Lys	Val	Val	Leu
	50					55					60				
Gly	Asn	Asp	Ala	Thr	Phe	Glu	Ile	Thr	Tyr	Glu	Ala	Phe	Glu	Pro	His
65					70					75					80
Ser	Ser	Tyr	Ser	Glu	Pro	Leu	Val	Lys	Lys	Arg	Ala	Val	Leu	Leu	Thr
				85					90					95	
Pro	Leu	Asn	Pro	Asp	Tyr	Thr	Phe	Glu	Asn	Phe	Val	Val	Gly	Pro	Gly
			100					105					110		
Asn	Ser	Phe	Ala	Tyr	His	Ala	Ala	Leu	Glu	Val	Ala	Lys	His	Pro	Gly
		115					120					125			
Arg	Tyr	Asn	Pro	Leu	Phe	Ile	Tyr	Gly	Gly	Val	Gly	Leu	Gly	Lys	Thr
	130					135					140				
His	Leu	Leu	Gln	Ser	Ile	Gly	Asn	Tyr	Val	Val	Gln	Asn	Glu	Pro	Asp
145					150					155					160
Leu	Arg	Val	Met	Tyr	Ile	Thr	Ser	Glu	Lys	Phe	Leu	Asn	Asp	Leu	Val
				165					170					175	
Asp	Ser	Met	Lys	Glu	Gly	Lys	Leu	Asn	Glu	Phe	Arg	Glu	Lys	Tyr	Arg
			180					185					190		
Lys	Lys	Val	Asp	Ile	Leu	Leu	Ile	Asp	Asp	Val	Gln	Phe	Leu	Ile	Gly
		195					200					205			
Lys	Thr	Gly	Val	Gln	Thr	Glu	Leu	Phe	His	Thr	Phe	Asn	Glu	Leu	His
	210					215					220				
Asp	Ser	Gly	Lys	Gln	Ile	Val	Ile	Cys	Ser	Asp	Arg	Glu	Pro	Gln	Lys
225					230					235					240
Leu	Ser	Glu	Phe	Gln	Asp	Arg	Leu	Val	Ser	Arg	Phe	Gln	Met	Gly	Leu
				245					250					255	
Val	Ala	Lys	Leu	Glu	Pro	Pro	Asp	Glu	Glu	Thr	Arg	Lys	Ser	Ile	Ala
			260					265					270		
Arg	Lys	Met	Leu	Glu	Ile	Glu	His	Gly	Glu	Leu	Pro	Glu	Glu	Val	Leu
		275					280					285			
Asn	Phe	Val	Ala	Glu	Asn	Val	Asp	Asp	Asn	Leu	Arg	Arg	Leu	Arg	Gly
						295					300				
Ala	Ile	Ile	Lys	Leu	Leu	Val	Tyr	Lys	Glu	Thr	Thr	Gly	Lys	Glu	Val
305					310					315					320
Asp	Leu	Lys	Glu	Ala	Ile	Leu	Leu	Leu	Lys	Asp	Phe	Ile	Lys	Pro	Asn
				325					330					335	
Arg	Val	Lys	Ala	Met	Asp	Pro	Ile	Asp	Glu	Leu	Ile	Glu	Ile	Val	Ala
			340					345					350		
Lys	Val	Thr	Gly	Val	Pro	Arg	Glu	Glu	Ile	Leu	Ser	Asn	Ser	Arg	Asn

355

360

365

Val	Lys	Ala	Leu	Thr	Ala	Arg	Arg	Ile	Gly	Met	Tyr	Val	Ala	Lys	Asn
370						375					380				
Tyr	Leu	Lys	Ser	Ser	Leu	Arg	Thr	Ile	Ala	Glu	Lys	Phe	Asn	Arg	Ser
385					390					395					400
His	Pro	Val	Val	Val	Asp	Ser	Val	Lys	Lys	Val	Lys	Asp	Ser	Leu	Leu
				405					410					415	
Lys	Gly	Asn	Lys	Gln	Leu	Lys	Ala	Leu	Ile	Asp	Glu	Val	Ile	Gly	Glu
		420						425						430	
Ile	Ser	Arg	Arg	Ala	Leu	Ser	Gly								
		435					440								

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Met	Asp	Thr	Asn	Asn	Asn	Ile	Glu	Lys	Glu	Ile	Leu	Ala	Leu	Val	Lys
1				5			10							15	
Gln	Asn	Pro	Lys	Val	Ser	Leu	Ile	Glu	Tyr	Glu	Asn	Tyr	Phe	Ser	Gln
			20					25					30		
Leu	Lys	Tyr	Asn	Pro	Asn	Ala	Ser	Lys	Ser	Asp	Ile	Ala	Phe	Phe	Tyr
		35					40					45			
Ala	Pro	Asn	Gln	Val	Leu	Cys	Thr	Thr	Ile	Thr	Ala	Lys	Tyr	Gly	Ala
	50					55					60				
Leu	Leu	Lys	Glu	Ile	Leu	Ser	Gln	Asn	Lys	Val	Gly	Met	His	Leu	Ala
65					70					75					80
His	Ser	Val	Asp	Val	Arg	Ile	Glu	Val	Ala	Pro	Lys	Ile	Gln	Ile	Asn
				85					90					95	
Ala	Gln	Ser	Asn	Ile	Asn	Tyr	Lys	Ala	Ile	Lys	Thr	Ser	Val	Lys	Asp
			100					105					110		
Ser	Tyr	Thr	Phe	Glu	Asn	Phe	Val	Val	Gly	Ser	Cys	Asn	Asn	Thr	Val
		115					120					125			
Tyr	Glu	Ile	Ala	Lys	Lys	Val	Ala	Gln	Ser	Asp	Thr	Pro	Pro	Tyr	Asn
	130					135					140				
Pro	Val	Leu	Phe	Tyr	Gly	Gly	Thr	Gly	Leu	Gly	Lys	Thr	His	Ile	Leu
145					150					155					160
Asn	Ala	Ile	Gly	Asn	His	Ala	Leu	Glu	Lys	His	Lys	Lys	Val	Val	Leu

008T80"8T24950

165

170

175

Val	Thr	Ser	Glu	Asp	Phe	Leu	Thr	Asp	Phe	Leu	Lys	His	Leu	Asp	Asn
			180					185					190		
Lys	Thr	Met	Asp	Ser	Phe	Lys	Ala	Lys	Tyr	Arg	His	Cys	Asp	Phe	Phe
		195					200					205			
Leu	Leu	Asp	Asp	Ala	Gln	Phe	Leu	Gln	Gly	Lys	Pro	Lys	Leu	Glu	Glu
	210					215					220				
Glu	Phe	Phe	His	Thr	Phe	Asn	Glu	Leu	His	Ala	Asn	Ser	Lys	Gln	Ile
225					230					235					240
Val	Leu	Ile	Ser	Asp	Arg	Ser	Pro	Lys	Asn	Ile	Ala	Gly	Leu	Glu	Asp
				245					250					255	
Arg	Leu	Lys	Ser	Arg	Phe	Glu	Trp	Gly	Ile	Thr	Ala	Lys	Val	Met	Pro
			260					265					270		
Pro	Asp	Leu	Glu	Thr	Lys	Leu	Ser	Ile	Val	Lys	Gln	Lys	Cys	Gln	Leu
		275					280					285			
Asn	Gln	Ile	Thr	Leu	Pro	Glu	Glu	Val	Met	Glu	Tyr	Ile	Ala	Gln	His
	290					295					300				
Ile	Ser	Asp	Asn	Ile	Arg	Gln	Met	Glu	Gly	Ala	Ile	Ile	Lys	Ile	Ser
305					310					315					320
Val	Asn	Ala	Asn	Leu	Met	Asn	Ala	Ser	Ile	Asp	Leu	Asn	Leu	Ala	Lys
				325					330					335	
Thr	Val	Leu	Glu	Asp	Leu	Gln	Lys	Asp	His	Ala	Glu	Gly	Ser	Ser	Leu
			340					345					350		
Glu	Asn	Ile	Leu	Leu	Ala	Val	Ala	Gln	Ser	Leu	Asn	Leu	Lys	Ser	Ser
		355					360					365			
Glu	Ile	Lys	Val	Ser	Ser	Arg	Gln	Lys	Asn	Val	Ala	Leu	Ala	Arg	Lys
	370					375					380				
Leu	Val	Val	Tyr	Phe	Ala	Arg	Leu	Tyr	Thr	Pro	Asn	Pro	Thr	Leu	Ser
385					390					395					400
Leu	Ala	Gln	Phe	Leu	Asp	Leu	Lys	Asp	His	Ser	Ser	Ile	Ser	Lys	Met
				405					410					415	
Tyr	Ser	Gly	Val	Lys	Lys	Met	Leu	Glu	Glu	Glu	Lys	Ser	Pro	Phe	Val
			420					425					430		
Leu	Ser	Leu	Arg	Glu	Glu	Ile	Lys	Asn	Arg	Leu	Asn	Glu	Leu	Asn	Asp
		435					440					445			
Lys	Lys	Thr	Ala	Phe	Asn	Ser	Ser	Glu							
	450					455									

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

09642218.031800

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GTGTGCGCACG AGGCCGTCTG GCAACACGTT CTGGAGCACA TCCGCCGCAG CATCACCGAG 60
GTGGAGTTCC ACACCTGGTT TGAAAGGATC CGCCCCTTGG GGATCCGGA CGGGGTGCTG 120
GAGCTCGCCG TGGCCACCTC CTTTGCCCTG GACTGGATCC GGCGCCACTA CGCCGGCCTC 180
ATCCAGGAGG GCCCTCGGCT CCTCGGGGCC CAGGCGCCCC GGTTCGAGCT CCGGGTGGTG 240
CCCCGGGTCG TAGTCCAGGA GGACATCTTC CAGCCCCCGC CGAGCCCCCC GGCCCAAGCT 300
CAACCCGAAG ATACCTTTAA AACTTCGTGG TGGGGCCCCA CAACTCCATG GCCCCACGGC 360
GGCGCCGTGG CCGTGGCCGA GTCCCCCGGC CGGGCCTACA ACCCCCTCTT CATCTACGGG 420
GGCCGTGGCC TGGGAAAGAC CTACCTGATG CACGCGGTGG GCCCACTCCG TGCGAAGCGC 480
TTCCCCACA TGAGATTAGA GTACGTTTCC ACGGAAACTT TCACCAACGA GCTCATCAAC 540
CGGCCATCCG CGAGGGACCG GATGACGGAG TTCCGGGAGC GGTACCGCTC CGTGGACCTC 600
CTGCTGGTGG ACGACGTCCA GTTCATCGCC GGAAAGGAGC GCACCCAGGA GGAGTTTTTC 660
CACACCTTCA ACGCCCTTTA CGAGGCCCCAC AAGCAGATCA TCCTCTCCTC CGACCGGCCG 720
CCCAAGGACA TCCTCACCTT GGAGGCGCGC CTGCGGAGCC GCTTTGAGTG GGGCCTGATC 780
ACCGACAATC CAGCCCCCGA CCTGGAAACC CGGATCGCCA TCCTGAAGAT GAACGCCAGC 840
AGCGGGCCTG AGGATCCCGA GGACGCCCTG GAGTACATCG CCCGGCAGGT CACCTCCAAC 900
ATCCGGGAGT GGGAAGGGGC CCTCATGCGG GCATCGCCTT TCGCCTCCCT CAACGGCGTT 960
GAGCTGACCC GCGCCGTGGC GGCCAAGGCT CTCCGACATC TTCGCCCCAG GGAGCTGGAG 1020
GCGGACCCCT TGGAGATCAT CCGCAAAGCG GCGGGACCAG TTCGGCCTGA AACCCCGGGA 1080
GGAGCTCACG GGGAGCGCCG CAAGAAGGAG GTGGTCCTCC CCCGGCAGCT CGCCATGTAC 1140
CTGGTGCGGG AGCTCACCCC GGCCTCCCTG CCCGAGATCG ACCAGCTCAA CGACGACCGG 1200
GACCACACCA CGGTCCTCTA CGCCATCCAG AAGGTCCAGG AGCTCGCGGA AAGCGACCGG 1260
GAGGTGCAGG GCCTCCTCCG CACCCTCCGG GAGGCGTGCA CATGA 1305

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

003789" 87224350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Val	Ser	His	Glu	Ala	Val	Trp	Gln	His	Val	Leu	Glu	His	Ile	Arg	Arg	
1				5					10					15		
Ser	Ile	Thr	Glu	Val	Glu	Phe	His	Thr	Trp	Phe	Glu	Arg	Ile	Arg	Pro	
			20					25					30			
Leu	Gly	Ile	Arg	Asp	Gly	Val	Leu	Glu	Leu	Ala	Val	Pro	Thr	Ser	Phe	
		35					40					45				
Ala	Leu	Asp	Trp	Ile	Arg	Arg	His	Tyr	Ala	Gly	Leu	Ile	Gln	Glu	Gly	
	50					55					60					
Pro	Arg	Leu	Leu	Gly	Ala	Gln	Ala	Pro	Arg	Phe	Glu	Leu	Arg	Val	Val	
65				70					75					80		
Pro	Gly	Val	Val	Val	Gln	Glu	Asp	Ile	Phe	Gln	Pro	Pro	Pro	Ser	Pro	
				85					90					95		
Pro	Ala	Gln	Ala	Gln	Pro	Glu	Asp	Thr	Phe	Lys	Thr	Ser	Trp	Trp	Gly	
			100					105					110			
Pro	Thr	Thr	Pro	Trp	Pro	His	Gly	Gly	Ala	Val	Ala	Val	Ala	Glu	Ser	
		115					120					125				
Pro	Gly	Arg	Ala	Tyr	Asn	Pro	Leu	Phe	Ile	Tyr	Gly	Gly	Arg	Gly	Leu	
	130				135						140					
Gly	Lys	Thr	Tyr	Leu	Met	His	Ala	Val	Gly	Pro	Leu	Arg	Ala	Lys	Arg	
145					150					155					160	
Phe	Pro	His	Met	Arg	Leu	Glu	Tyr	Val	Ser	Thr	Glu	Thr	Phe	Thr	Asn	
			165						170					175		
Glu	Leu	Ile	Asn	Arg	Pro	Ser	Ala	Arg	Asp	Arg	Met	Thr	Glu	Phe	Arg	
			180					185					190			
Glu	Arg	Tyr	Arg	Ser	Val	Asp	Leu	Leu	Leu	Val	Asp	Asp	Val	Gln	Phe	
		195					200					205				
Ile	Ala	Gly	Lys	Glu	Arg	Thr	Gln	Glu	Glu	Phe	Phe	His	Thr	Phe	Asn	
	210					215					220					
Ala	Leu	Tyr	Glu	Ala	His	Lys	Gln	Ile	Ile	Leu	Ser	Ser	Asp	Arg	Pro	
225					230					235					240	
Pro	Lys	Asp	Ile	Leu	Thr	Leu	Glu	Ala	Arg	Leu	Arg	Ser	Arg	Phe	Glu	
			245						250					255		
Trp	Gly	Leu	Ile	Thr	Asp	Asn	Pro	Ala	Pro	Asp	Leu	Glu	Thr	Arg	Ile	
			260					265					270			
Ala	Ile	Leu	Lys	Met	Asn	Ala	Ser	Ser	Gly	Pro	Glu	Asp	Pro	Glu	Asp	
		275					280					285				
Ala	Leu	Glu	Tyr	Ile	Ala	Arg	Gln	Val	Thr	Ser	Asn	Ile	Arg	Glu	Trp	
	290					295					300					
Glu	Gly	Ala	Leu	Met	Arg	Ala	Ser	Pro	Phe	Ala	Ser	Leu	Asn	Gly	Val	
305					310					315					320	

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Glu Leu Thr Arg Ala Val Ala Ala Lys Ala Leu Arg His Leu Arg Pro
 325 330 335
 Arg Glu Leu Glu Ala Asp Pro Leu Glu Ile Ile Arg Lys Ala Ala Gly
 340 345 350
 Pro Val Arg Pro Glu Thr Pro Gly Gly Ala His Gly Glu Arg Arg Lys
 355 360 365
 Lys Glu Val Val Leu Pro Arg Gln Leu Ala Met Tyr Leu Val Arg Glu
 370 375 380
 Leu Thr Pro Ala Ser Leu Pro Glu Ile Asp Gln Leu Asn Asp Asp Arg
 385 390 395 400
 Asp His Thr Thr Val Leu Tyr Ala Ile Gln Lys Val Gln Glu Leu Ala
 405 410 415
 Glu Ser Asp Arg Glu Val Gln Gly Leu Leu Arg Thr Leu Arg Glu Ala
 420 425 430
 Cys Thr

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1128 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

ATGAACATAA CGGTTCCCAA AAAACTCCTC TCGGACCAGC TTTCCCTCCT GGAGCGCATC	60
GTCCCCTCTA GAAGCGCCAA CCCCTCTAC ACCTACCTGG GGCTTTACGC CGAGGAAGGG	120
GCCTTGATCC TCTTCGGGAC CAACGGGGAG GTGGACCTCG AGGTCCGCCT CCCC GCCGAG	180
GCCCAAAGCC TTCCCCGGGT GCTCGTCCCC GCCAGCCCT TCTTCCAGCT GGTGCGGAGC	240
CTTCCTGGGG ACCTCGTGGC CCTCGGCCCT GCCTCGGAGC CGGGCCAGGG GGGGCAGCTG	300
GAGCTCTCCT CCGGGCGTTT CCGCACCCGG CTCAGCCTGG CCCCTGCCGA GGGCTACCCC	360
GAGCTTCTGG TGCCCCAGGG GGAGGACAAG GGGGCCTTCC CCCTCCGGAC GCGGATGCCC	420
TCCGGGGAGC TCGTCAAGGC CTTGACCCAC GTGCGCTACG CCGCGAGCAA CGAGGAGTAC	480
CGGGCCATCT TCCGCGGGGT GCAGCTGGAG TTCTCCCCC AGGGCTTCCG GGCGGTGGCC	540
TCCGACGGGT ACCGCCTCGC CCTCTACGAC CTGCCCCCTGC CCCAAGGGTT CCAGGCCAAG	600
GCCGTGGTCC CCGCCCGGAG CGTGGACGAG ATGGTGCGGG TCCTGAAGGG GGCGGACGGG	660
GCCGAGGCCG TCCTCGCCCT GGGCGAGGGG GTGTTGGCCC TGGCCCTCGA GGGCGGAAGC	720

0034230" 27224350

GGGGTCCGGA TGGCCCTCCG CCTCATGGAA GGGGAGTTCC CCGACTACCA GAGGGTCATC 780
 CCCCAGGAGT TCGCCCTCAA GGTCCAGGTG GAGGGGGAGG CCCTCAGGGA GGCGGTGCGC 840
 CGGGTGAGCG TCCTCTCCGA CCGGCAGAAC CACCGGGTGG ACCTCCTTTT GGAGGAAGGC 900
 CGGATCCTCC TCTCCGCCGA GGGGGACTAC GGCAAGGGGC AGGAGGAGGT GCCCCCCCAG 960
 GTGGAGGGGC CGGACATGGC CGTGGCCTAC AACGCCCCGCT ACCTCCTCGA GGCCCTCGCC 1020
 CCCGTGGGGG ACCGGGCCCCA CCTGGGCATC TCCGGGCCCA CGAGCCCGAG CCTCATCTGG 1080
 GGGGACGGGG AGGGGTACCG GGCGGTGGTG GTGCCCCCTCA GGGTCTAG 1128

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 376 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Met	Asn	Ile	Thr	Val	Pro	Lys	Lys	Leu	Leu	Ser	Asp	Gln	Leu	Ser	Leu	1	5	10	15
Leu	Glu	Arg	Ile	Val	Pro	Ser	Arg	Ser	Ala	Asn	Pro	Leu	Tyr	Thr	Tyr	20	25	30	
Leu	Gly	Leu	Tyr	Ala	Glu	Glu	Gly	Ala	Leu	Ile	Leu	Phe	Gly	Thr	Asn	35	40	45	
Gly	Glu	Val	Asp	Leu	Glu	Val	Arg	Leu	Pro	Ala	Glu	Ala	Gln	Ser	Leu	50	55	60	
Pro	Arg	Val	Leu	Val	Pro	Ala	Gln	Pro	Phe	Phe	Gln	Leu	Val	Arg	Ser	65	70	75	80
Leu	Pro	Gly	Asp	Leu	Val	Ala	Leu	Gly	Leu	Ala	Ser	Glu	Pro	Gly	Gln	85	90	95	
Gly	Gly	Gln	Leu	Glu	Leu	Ser	Ser	Gly	Arg	Phe	Arg	Thr	Arg	Leu	Ser	100	105	110	
Leu	Ala	Pro	Ala	Glu	Gly	Tyr	Pro	Glu	Leu	Leu	Val	Pro	Glu	Gly	Glu	115	120	125	
Asp	Lys	Gly	Ala	Phe	Pro	Leu	Arg	Thr	Arg	Met	Pro	Ser	Gly	Glu	Leu	130	135	140	
Val	Lys	Ala	Leu	Thr	His	Val	Arg	Tyr	Ala	Ala	Ser	Asn	Glu	Glu	Tyr	145	150	155	160
Arg	Ala	Ile	Phe	Arg	Gly	Val	Gln	Leu	Glu	Phe	Ser	Pro	Gln	Gly	Phe	165	170	175	

00642218 001800

Arg	Ala	Val	Ala 180	Ser	Asp	Gly	Tyr	Arg 185	Leu	Ala	Leu	Tyr	Asp 190	Leu	Pro
Leu	Pro	Gln 195	Gly	Phe	Gln	Ala	Lys 200	Ala	Val	Val	Pro	Ala 205	Arg	Ser	Val
Asp	Glu 210	Met	Val	Arg	Val	Leu 215	Lys	Gly	Ala	Asp	Gly 220	Ala	Glu	Ala	Val
Leu 225	Ala	Leu	Gly	Glu	Gly 230	Val	Leu	Ala	Leu	Ala 235	Leu	Glu	Gly	Gly	Ser 240
Gly	Val	Arg	Met	Ala 245	Leu	Arg	Leu	Met	Glu 250	Gly	Glu	Phe	Pro	Asp 255	Tyr
Gln	Arg	Val	Ile 260	Pro	Gln	Glu	Phe	Ala 265	Leu	Lys	Val	Gln	Val 270	Glu	Gly
Glu	Ala 275	Leu	Arg	Glu	Ala	Val	Arg 280	Arg	Val	Ser	Val	Leu 285	Ser	Asp	Arg
Gln 290	Asn	His	Arg	Val	Asp	Leu 295	Leu	Leu	Glu	Glu	Gly 300	Arg	Ile	Leu	Leu
Ser 305	Ala	Glu	Gly	Asp	Tyr 310	Gly	Lys	Gly	Gln	Glu 315	Glu	Val	Pro	Ala	Gln 320
Val	Glu	Gly	Pro	Asp 325	Met	Ala	Val	Ala	Tyr 330	Asn	Ala	Arg	Tyr	Leu 335	Leu
Glu	Ala	Leu 340	Ala	Pro	Val	Gly	Asp	Arg 345	Ala	His	Leu	Gly	Ile 350	Ser	Gly
Pro	Thr 355	Ser	Pro	Ser	Leu	Ile	Trp 360	Gly	Asp	Gly	Glu	Gly 365	Tyr	Arg	Ala
Val 370	Val	Val	Pro	Leu	Arg	Val 375	Glx								

(2) INFORMATION FOR SEQ ID NO:108:

- (A) LENGTH: 376 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Gly Glu Val Asp Leu Glu Val Arg Leu Pro Ala Glu Ala Gln Ser Leu
 50 55 60
 Pro Arg Val Leu Val Pro Ala Gln Pro Phe Phe Gln Leu Val Arg Ser
 65 70 75 80
 Leu Pro Gly Asp Leu Val Ala Leu Gly Leu Ala Ser Glu Pro Gly Gln
 85 90 95
 Gly Gly Gln Leu Glu Leu Ser Ser Gly Arg Phe Arg Thr Arg Leu Ser
 100 105 110
 Leu Ala Pro Ala Glu Gly Tyr Pro Glu Leu Leu Val Pro Glu Gly Glu
 115 120 125
 Asp Lys Gly Ala Phe Pro Leu Arg Thr Arg Met Pro Ser Gly Glu Leu
 130 135 140
 Val Lys Ala Leu Thr His Val Arg Tyr Ala Ala Ser Asn Glu Glu Tyr
 145 150 155 160
 Arg Ala Ile Phe Arg Gly Val Gln Leu Glu Phe Ser Pro Gln Gly Phe
 165 170 175
 Arg Ala Val Ala Ser Asp Gly Tyr Arg Leu Ala Leu Tyr Asp Leu Pro
 180 185 190
 Leu Pro Gln Gly Phe Gln Ala Lys Ala Val Val Pro Ala Arg Ser Val
 195 200 205
 Asp Glu Met Val Arg Val Leu Lys Gly Ala Asp Gly Ala Glu Ala Val
 210 215 220
 Leu Ala Leu Gly Glu Gly Val Leu Ala Leu Ala Leu Glu Gly Gly Ser
 225 230 235 240
 Gly Val Arg Met Ala Leu Arg Leu Met Glu Gly Glu Phe Pro Asp Tyr
 245 250 255
 Gln Arg Val Ile Pro Gln Glu Phe Ala Leu Lys Val Gln Val Glu Gly
 260 265 270
 Glu Ala Leu Arg Glu Ala Val Arg Arg Val Ser Val Leu Ser Asp Arg
 275 280 285
 Gln Asn His Arg Val Asp Leu Leu Leu Glu Glu Gly Arg Ile Leu Leu
 290 295 300
 Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln
 305 310 315 320
 Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu
 325 330 335
 Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly
 340 345 350
 Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala
 355 360 365
 Val Val Val Pro Leu Arg Val Glx
 370 375

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(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Met Lys Phe Thr Val Glu Arg Glu His Leu Leu Lys Pro Leu Gln Gln
1 5 10 15
Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn
20 25 30
Leu Leu Leu Gln Val Ala Asp Gly Thr Leu Ser Leu Thr Gly Thr Asp
35 40 45
Leu Glu Met Glu Met Val Ala Arg Val Ala Leu Val Gln Pro His Glu
50 55 60
Pro Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Cys Arg
65 70 75 80
Gly Leu Pro Glu Gly Ala Glu Ile Ala Val Gln Leu Glu Gly Glu Arg
85 90 95
Met Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro
100 105 110
Ala Ala Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe
115 120 125
Thr Leu Pro Gln Ala Thr Met Lys Arg Leu Ile Glu Ala Thr Gln Phe
130 135 140
Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe
145 150 155 160
Glu Thr Glu Gly Glu Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg
165 170 175
Leu Ala Val Cys Ser Met Pro Ile Gly Gln Ser Leu Pro Ser His Ser
180 185 190
Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Met Leu Asp
195 200 205
Gly Gly Asp Asn Pro Leu Arg Val Gln Ile Gly Ser Asn Asn Ile Arg
210 215 220
Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly Arg
225 230 235 240
Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Asp Lys His Leu
245 250 255

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Glu Ala Gly Cys Asp Leu Leu Lys Gln Ala Phe Ala Arg Ala Ala Ile
 260 265 270
 Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Leu Tyr Val Ser Glu Asn
 275 280 285
 Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu Glu
 290 295 300
 Ile Leu Asp Val Thr Tyr Ser Gly Ala Glu Met Glu Ile Gly Phe Asn
 305 310 315 320
 Val Ser Tyr Val Leu Asp Val Leu Asn Ala Leu Lys Cys Glu Asn Val
 325 330 335
 Arg Met Met Leu Thr Asp Ser Val Ser Ser Val Gln Ile Glu Asp Ala
 340 345 350
 Ala Ser Gln Ser Ala Ala Tyr Val Val Met Pro Met Arg Leu Glx
 355 360 365

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Lys Phe Ile Ile Glu Arg Glu Gln Leu Leu Lys Pro Leu Gln Gln
 1 5 10 15
 Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn
 20 25 30
 Leu Leu Leu Lys Val Thr Glu Asn Thr Leu Ser Leu Thr Gly Thr Asp
 35 40 45
 Leu Glu Met Glu Met Met Ala Arg Val Ser Leu Ser Gln Ser His Glu
 50 55 60
 Ile Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Trp Arg
 65 70 75 80
 Gly Leu Pro Glu Gly Ala Glu Ile Ser Val Glu Leu Asp Gly Asp Arg
 85 90 95
 Leu Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro
 100 105 110
 Ala Ser Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe
 115 120 125
 Thr Leu Pro Gln Ala Thr Leu Lys Arg Leu Ile Glu Ser Thr Gln Phe
 130 135 140

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Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe
 145 150 155 160
 Glu Thr Glu Asn Thr Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg
 165 170 175
 Leu Ala Val Cys Ala Met Asp Ile Gly Gln Ser Leu Pro Gly His Ser
 180 185 190
 Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Leu Leu Asp
 195 200 205
 Gly Ser Gly Glu Ser Leu Leu Gln Leu Gln Ile Gly Ser Asn Asn Leu
 210 215 220
 Arg Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly
 225 230 235 240
 Arg Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Thr Lys Thr
 245 250 255
 Val Ile Ala Gly Cys Asp Ile Leu Lys Gln Ala Phe Ser Arg Ala Ala
 260 265 270
 Ile Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Ile Asn Leu Thr Asn
 275 280 285
 Gly Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu
 290 295 300
 Glu Ile Val Asp Val Gln Tyr Gln Gly Glu Glu Met Glu Ile Gly Phe
 305 310 315 320
 Asn Val Ser Tyr Leu Leu Asp Val Leu Asn Thr Leu Lys Cys Glu Glu
 325 330 335
 Val Lys Leu Leu Leu Thr Asp Ala Val Ser Ser Val Gln Val Glu Asn
 340 345 350
 Val Ala Ser Ala Ala Ala Tyr Val Val Met Pro Met Arg Leu
 355 360 365

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Met Gln Phe Ser Ile Ser Arg Glu Asn Leu Leu Lys Pro Leu Gln Gln
 1 5 10 15
 Val Cys Gly Val Leu Ser Asn Arg Pro Asn Ile Pro Val Leu Asn Asn
 20 25 30

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Val	Leu	Leu	Gln	Ile	Glu	Asp	Tyr	Arg	Leu	Thr	Ile	Thr	Gly	Thr	Asp	35	40	45
Leu	Glu	Val	Glu	Leu	Ser	Ser	Gln	Thr	Gln	Leu	Ser	Ser	Ser	Ser	Glu	50	55	60
Asn	Gly	Thr	Phe	Thr	Ile	Pro	Ala	Lys	Lys	Phe	Leu	Asp	Ile	Cys	Arg	65	70	75
Thr	Leu	Ser	Asp	Asp	Ser	Glu	Ile	Thr	Val	Thr	Phe	Glu	Gln	Asp	Arg	85	90	95
Ala	Leu	Val	Gln	Ser	Gly	Arg	Ser	Arg	Phe	Thr	Leu	Ala	Thr	Gln	Pro	100	105	110
Ala	Glu	Glu	Tyr	Pro	Asn	Leu	Thr	Asp	Trp	Gln	Ser	Glu	Val	Asp	Phe	115	120	125
Glu	Leu	Pro	Gln	Asn	Thr	Leu	Arg	Arg	Leu	Ile	Glu	Ala	Thr	Gln	Phe	130	135	140
Ser	Met	Ala	Asn	Gln	Asp	Ala	Arg	Tyr	Phe	Leu	Asn	Gly	Met	Lys	Phe	145	150	155
Glu	Thr	Glu	Gly	Asn	Leu	Leu	Arg	Thr	Val	Ala	Thr	Asp	Gly	His	Arg	165	170	175
Leu	Ala	Val	Cys	Thr	Ile	Ser	Leu	Glu	Gln	Glu	Leu	Gln	Asn	His	Ser	180	185	190
Val	Ile	Leu	Pro	Arg	Lys	Gly	Val	Leu	Glu	Leu	Val	Arg	Leu	Leu	Glu	195	200	205
Thr	Asn	Asp	Glu	Pro	Ala	Arg	Leu	Gln	Ile	Gly	Thr	Asn	Asn	Leu	Arg	210	215	220
Val	His	Leu	Lys	Asn	Thr	Val	Phe	Thr	Ser	Lys	Leu	Ile	Asp	Gly	Arg	225	230	235
Phe	Pro	Asp	Tyr	Arg	Arg	Val	Leu	Pro	Arg	Asn	Ala	Thr	Lys	Ile	Val	245	250	255
Glu	Gly	Asn	Trp	Glu	Met	Leu	Lys	Gln	Ala	Phe	Ala	Arg	Ala	Ser	Ile	260	265	270
Leu	Ser	Asn	Glu	Arg	Ala	Arg	Ser	Val	Arg	Leu	Ser	Leu	Lys	Glu	Asn	275	280	285
Gln	Leu	Lys	Ile	Thr	Ala	Ser	Asn	Thr	Glu	His	Glu	Glu	Ala	Glu	Glu	290	295	300
Ile	Val	Asp	Val	Asn	Tyr	Asn	Gly	Glu	Glu	Leu	Glu	Val	Gly	Phe	Asn	305	310	315
Val	Thr	Tyr	Ile	Leu	Asp	Val	Leu	Asn	Ala	Leu	Lys	Cys	Asn	Gln	Val	325	330	335
Arg	Met	Cys	Leu	Thr	Asp	Ala	Phe	Ser	Ser	Cys	Leu	Ile	Glu	Asn	Cys	340	345	350
Glu	Asp	Ser	Ser	Cys	Glu	Tyr	Val	Ile	Met	Pro	Met	Arg	Leu			355	360	365

[illegible]

(A) LENGTH: 367 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Val Ala Gly Val Val Glu Arg Arg Gln Thr Leu Pro Val Leu Ser Asn
20 25 30

Val Leu Leu Val Val Gln Gly Gln Gln Leu Ser Leu Thr Gly Thr Asp
35 40 45

Leu Glu Val Glu Leu Val Gly Arg Val Gln Leu Glu Glu Pro Ala Glu
50 55 60

Pro Gly Glu Ile Thr Val Pro Ala Arg Lys Leu Met Asp Ile Cys Lys
65 70 75 80

Ser Leu Pro Asn Asp Ala Leu Ile Asp Ile Lys Val Asp Glu Gln Lys
85 90 95

Leu Leu Val Lys Ala Gly Arg Ser Arg Phe Thr Leu Ser Thr Leu Pro
100 105 110

Ala Asn Asp Phe Pro Thr Val Glu Glu Gly Pro Gly Ser Leu Thr Cys
115 120 125

Asn Leu Glu Gln Ser Lys Leu Arg Arg Leu Ile Glu Arg Thr Ser Phe
130 135 140

Ala Met Ala Gln Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Leu .
145 150 155 160

Glu Val Ser Arg Asn Thr Leu Arg Ala Val Ser Thr Asp Gly His Arg
165 170 175

Leu Ala Leu Cys Ser Met Ser Ala Pro Ile Glu Gln Glu Asp Arg His
180 185 190

Gln Val Ile Val Pro Arg Lys Gly Ile Leu Glu Leu Ala Arg Leu Leu
195 200 205

Thr Asp Pro Glu Gly Met Val Ser Ile Val Leu Gly Gln His His Ile
210 215 220

Arg Ala Thr Thr Gly Glu Phe Thr Phe Thr Ser Lys Leu Val Asp Gly
225 230 235 240

Lys Phe Pro Asp Tyr Glu Arg Val Leu Pro Lys Gly Gly Asp Lys Leu
245 250 255

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(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

Met 1	Lys	Phe	Thr	Ile 5	Gln	Asn	Asp	Ile	Leu 10	Thr	Lys	Asn	Leu	Lys 15	Lys
Ile	Thr	Arg	Val 20	Leu	Val	Lys	Asn	Ile 25	Ser	Phe	Pro	Ile	Leu 30	Glu	Asn
Ile	Leu	Ile 35	Gln	Val	Glu	Asp	Gly 40	Thr	Leu	Ser	Leu	Thr 45	Thr	Thr	Asn
Leu	Glu 50	Ile	Glu	Leu	Ile	Ser 55	Lys	Ile	Glu	Ile	Ile 60	Thr	Lys	Tyr	Ile
Pro 65	Gly	Lys	Thr	Thr 70	Ile	Ser	Gly	Arg	Lys	Ile 75	Leu	Asn	Ile	Cys	Arg 80
Thr	Leu	Ser	Glu	Lys 85	Ser	Lys	Ile	Lys	Met 90	Gln	Leu	Lys	Asn	Lys 95	Lys
Met	Tyr	Ile	Ser 100	Ser	Glu	Asn	Ser	Asn 105	Tyr	Ile	Leu	Ser	Thr 110	Leu	Ser
Ala	Asp	Thr 115	Phe	Pro	Asn	His	Gln 120	Asn	Phe	Asp	Tyr	Ile 125	Ser	Lys	Phe
Asp	Ile 130	Ser	Ser	Asn	Ile	Leu 135	Lys	Glu	Met	Ile	Glu 140	Lys	Thr	Glu	Phe

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "PRIMER"

- (iii) HYPOTHETICAL: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GTGTGGATCC GTGGTGACCT TAGCCAC

27

- (2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "PRIMER"

- (iii) HYPOTHETICAL: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

TTCGTGTCCG AGGACCTTGT GGTCCACAAC

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